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OM protein - protein search, using sw model

Run on: January 11, 2006, 00:04:17 ; Search time 76 Seconds
(without alignments)
104.063 Million cell updates/sec

Title: US-10-031-008-7

Perfect score: 85

Sequence: 1 MRYMILGLLAALAAVCSAA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	18	4 AAB49610	Aab49610 Adenoviru
2	85	100.0	18	5 ABB79904	Abb79904 E3/19K si
3	85	100.0	18	6 ABU87174	Abu87174 Adenoviru
4	85	100.0	18	8 ADN00612	Adn00612 E3/19K si
5	85	100.0	18	8 ADO55472	Ado55472 Murine E3
6	85	100.0	18	8 ADO43914	Ado43914 Amino aci
7	85	100.0	27	2 AAR63153	Aar63153 PLA tumou
8	85	100.0	27	2 AAY05400	Aay05400 T-cell Be
9	85	100.0	28	2 AAW81051	Aaw81051 Signal pe
10	85	100.0	48	6 ABU87179	Abu87179 Expressio
11	85	100.0	56	6 ABU87178	Abu87178 Carbohydr
12	85	100.0	90	3 AAY44964	Aay44964 KDEBL rece
13	85	100.0	109	3 AAY44963	Aay44963 KDEBL rece
14	85	100.0	109	3 AAY44965	Aay44965 KDEBL rece
15	85	100.0	109	3 AAY44966	Aay44966 KDEBL rece
16	82	96.5	26	6 ADA37032	Ada37032 Adenovira
17	82	96.5	26	6 ADA37037	Ada37037 Minigene
18	81	95.3	17	2 AAR63147	Aar63147 Adenoviru
19	81	95.3	17	2 AAW81046	Aaw81046 Signal pe
20	81	95.3	17	3 AAY67363	Aay67363 Sorting s
21	81	95.3	27	2 AAW81049	Aaw81049 Signal pe
22	80	94.1	31	4 AAB35489	Aab35489 Internali
23	80	94.1	31	7 ADA88894	Ada88894 Internali
24	76	89.4	17	2 AAW81048	Aaw81048 Signal pe

25	76	89.4	27	2 AAW81052	Aaw81052 Signal pe
26	51	60.0	175	3 AAY70435	Aay70435 Haematobi
27	48	56.5	179	4 ABB64175	Abb64175 Drosophil
28	48	56.5	181	4 ABB67296	Abb67296 Drosophil
29	47	55.3	205	9 ABM94647	Abm94647 M. xanthu
30	47	55.3	305	7 ABO60854	Abo60854 Klebsiell
31	46	54.1	157	7 ABO73866	Abp73866 Pseudomon
32	46	54.1	456	5 ABP65422	Abp65422 Bifidobac
33	46	54.1	3117	3 AAY53667	Aay53667 Sequence
34	46	54.1	5175	8 ADN24208	Adn24208 Bacterial
35	46	54.1	5175	8 ADN24206	Adn24206 Bacterial
36	46	54.1	5198	8 ADN24207	Adn24207 Bacterial
37	46	54.1	5198	8 ADN24205	Adn24205 Bacterial
38	45	52.9	74	5 ABP01621	Abp01621 Human ORF
39	45	52.9	367	9 ABM95341	Abm95341 M. xanthu
40	45	52.9	3390	4 AAE07989	Aae07989 Wild-type
41	45	52.9	3390	4 AAE07990	Aae07990 Attenuate
42	45	52.9	3390	8 ADG93316	Adg93316 DEN3 (Sle
43	44	51.8	313	8 ADN72917	Adn72917 Thale cre
44	44	51.8	372	6 ABU50190	Abu50190 Protein e
45	44	51.8	406	8 ADY14032	Ady14032 Plant ful

ALIGNMENTS

RESULT 1

AAB49610

ID AAB49610 standard; peptide; 18 AA.

XX AAB49610;

XX AC

DT 02-MAR-2001 (first entry)

XX Adenovirus E19 signal peptide sequence.

XX Antiangiogenic protein; viral particle; antitumour; vulnery;

KW cytostatic; antidiabetic; antirheumatic; tumour; angiogenesis; leukaemia;

KW metastasis; rheumatic disease; diabetic neovascularisation;

KW haematopoiesis; wound healing; adenovirus; signal sequence.

XX Mastadenovirus.

OS

XX WC200068379-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US012392.

XX 07-MAY-1999; 99US-0133243P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Libutti SK, Feldman A;

XX WPI; 2001-016095/02.

XX Novel compounds comprising recombinant nucleic acid which can be packaged

PT in virus particles, and which encodes antiangiogenic protein inserted

PT within viral nucleic acid, useful for treating tumors, leukemia.

XX Claim 22; Page 54; 78pp; English.

XX This invention relates to a compound comprising a recombinant nucleic

CC acid sequence encoding an antiangiogenic protein (e.g. endostatin)

CC inserted within a viral nucleic acid sequence. The recombinant nucleic

CC acid sequence is packaged in a virus particle the expression of which

CC results in the production of the antiangiogenic protein. The compound has

CC antitumour; vulnery; cytostatic; antidiabetic; and antirheumatic

CC activity. The compound is useful for expressing an antiangiogenic protein

CC in a cell to treat a tumour. The compounds can also be used for treating

CC any disease or process mediated by angiogenesis such as leukaemia,

CC metastasis, rheumatic diseases, diabetic neovascularisation,

CC haematopoiesis and wound healing. The present sequence represents an
 CC Adenovirus E19 signal peptide. DNA encoding the peptide is used to direct
 CC expression of the antiangiogenic protein in cells containing the compound
 CC of the invention
 XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 85; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLAAVCSAA 18
 |||||
 DB 1 MRYMILGLLAAVCSAA 18

RESULT 2
 ABB79904
 ID ABB79904 standard; peptide; 18 AA.

XX AC ABB79904;

XX DT 05-DEC-2002 (first entry)

XX DE E3/19K signal peptide.

XX KW Endostatin; mouse; ophthalmological; ocular neovascularisation;
 KW choroidal neovascularisation; gene therapy; adenovirus; vector;
 KW signal peptide.

XX OS Mus musculus.

XX PN WO200267971-A2.

XX PD 06-SEP-2002.

XX PF 21-FEB-2002; 2002WO-US005336.

XX PR 22-FEB-2001; 2001US-0270787P.

XX PR 04-APR-2001; 2001US-0281296P.

XX XX (NOVS) NOVARTIS AG.

XX PI Brazzell RK, Campochiaro PA, Dixon KH;

XX PS WPI; 2002-698636/75.

XX PT Treating or preventing choroidal neovascularization comprises increasing
 PT the amount of endostatin in ocular tissues of afflicted individuals to a
 PT choroidal neovascularization inhibiting level.

XX PS Example 1; Page 19; 44pp; English.

XX CC The present sequence is that of the 18-amino acid E3/19K signal peptide.
 CC A nucleic acid encoding this signal peptide was inserted upstream of a
 CC murine endostatin coding sequence in the construction of an adenovirus
 CC vector. The viral vector was used to infect murine colon adenocarcinoma
 CC MC38 cells for production of endostatin. A claimed method for the
 CC treatment of ocular, especially choroidal, neovascularisation involves
 CC increasing the level of endostatin in ocular tissue, especially the level
 CC of human endostatin (see ABB79901). The increase is effected by
 CC administering a viral vector, especially an adenovirus, adeno-associated
 CC virus, a retrovirus or lentivirus vector, comprising an endostatin-
 CC encoding nucleic acid. Cells secreting endostatin may be encapsulated and
 CC implanted within an individual

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 85; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLAAVCSAA 18

DB 1 MRYMILGLLAAVCSAA 18
 |||||

RESULT 3

ABU87174

ID ABU87174 standard; peptide; 18 AA.

XX AC ABU87174;

XX DT 23-OCT-2003 (revised)

XX DT 03-JUL-2003 (first entry)

XX DE Adenovirus E3 leader sequence.

XX KW Carbohydrate antigen; mimotope; vaccine; infection; tumour; pathogen;

XX KW cytostatic; antibacterial; antigen; E3 leader sequence.

XX OS unidentified adenovirus.

XX PN US2003017497-A1.

XX PD 23-JAN-2003.

XX PF 28-JUN-2001; 2001US-00894594.

XX PR 04-FEB-1998; 98US-0073690P.

XX PR 04-FEB-1999; 99WO-US002405.

XX PR 28-JUN-2000; 2000US-0214517P.

XX PR 07-NOV-2000; 2000US-00601558.

XX PA (KIEB/) KIEBER-EMMONS T.

XX PA (WEIN/) WEINER D B.

XX PA (MONZ/) MONZAVI-KARBASSI B.

XX PI Kieber-Emmons T, Weiner DB, Monzavi-Karbassi B;

XX DR WPI; 2003-401670/38.

XX PT Preparing a recombinant antibody or peptide that mimics an antigenic
 PT carbohydrate, for generating an immune response against a pathogen,
 PT comprises identifying a peptide sequence that is cross reactive with an
 PT antigenic carbohydrate.

XX PS Example 9; Page 20; 75pp; English.

XX CC The invention relates to preparing a recombinant antibody or a peptide
 CC that mimics an antigenic carbohydrate comprising identifying a peptide
 CC sequence that is immunogenically cross reactive with an antigenic
 CC carbohydrate, and synthesising a recombinant antibody comprising the
 CC peptide sequence or a peptide comprising at least two repeating units of
 CC the peptide sequence. Also included are a method of generating an immune
 CC response against a pathogen or tumour cell in an individual (comprising
 CC administering to the individual the carbohydrate antigen peptide mimotope
 CC or antibody above, a DNA vaccine, live attenuated vaccine or recombinant
 CC vaccine comprising a nucleic acid sequence that encodes then peptides of
 CC the invention), a method of enhancing binding of anti-antigenic
 CC carbohydrate antibodies to the antigenic carbohydrate in an individual
 CC (comprising administering to the individual anti-antigenic carbohydrate
 CC antibodies and a peptide comprising 1-3 repeat units of a peptide
 CC sequence that mimics an antigenic carbohydrate), a method of inhibiting
 CC binding of a ligand to a receptor that is an antigenic carbohydrate using
 CC the peptides/antibodies of the invention and a method of identifying
 CC peptide sequences that can induce an immune response against two or more
 CC different pathogens (comprising identifying a peptide sequence that is
 CC immunogenically cross reactive with an antigenic carbohydrate, which is
 CC associated with a pathogen, administering a peptide comprising the
 CC peptide sequence to an animal to induce an immune response and analysing
 CC the immune response to identify two or more pathogens against which the
 CC immune response cross reacts. The peptides, antibodies and methods are
 CC useful for generating a prophylactic or therapeutic immune response
 CC against a tumour cell or a pathogen in an individual. The peptides are
 CC useful as immunogenic agents, vaccines, adjuvants, enhancers of antibody

CC binding, or inhibitors of receptor/ligand binding. The methods are also
CC useful for enhancing binding of anti-antigenic carbohydrate antibodies to
CC the antigenic carbohydrate in an individual, inhibiting binding of a
CC ligand to a receptor that is an antigenic carbohydrate, or identifying
CC peptide sequences that can induce an immune response. The mimotope
CC peptides may be expressed from a vector as a fusion protein with an
CC adenovirus E3 leader sequence and an HIV (human immunodeficiency virus) T
CC helper cell epitope. The present sequence is the adenovirus E3 leader
CC sequence. (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 85; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
| | | | | | | | | | | | | | | | | |
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 4
ADN00612
ID ADN00612 standard; peptide; 18 AA.

AC ADN00612;

DT 17-JUN-2004 (first entry)

DE E3/19K signal sequence, SEQ ID 13.

KW Retinal detachment; retinal edema; endostatin; ocular tissue;
KW ophthalmological; gene therapy.

XX unidentified adenovirus.

PN WO2004020469-A2.

PD 11-MAR-2004.

PF 27-AUG-2003; 2003WO-EP009497.

PR 28-AUG-2002; 2002US-0406470P.

XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS PHARMA GMBH.

XX Campochiaro PA, Kaleko M;

PI WPI; 2004-239158/22.

XX Treating retinal detachment or retinal edema in an individual comprises
PT increasing the amount of an endostatin in the ocular tissues of the
PT individual to a retinal detachment- or retinal edema-inhibiting amount.

XX Example 1; SEQ ID NO 13; 48pp; English.

XX The present invention relates to a method for treating retinal detachment
CC or retinal edema in an individual. The method comprises effecting an
CC increase in the amount of an endostatin (ADN00600 or ADN00602) in ocular
CC tissues of the individual to a retinal detachment- or retinal edema-
CC inhibiting amount. The endostatin is used in manufacturing a medicament
CC for the treatment of retinal detachment or retinal edema in an
CC individual. In an example from the invention, the murine endostatin gene
CC was cloned into the TA cloning vector. The E3/19K signal sequence
CC (ADN00612) was inserted upstream from the endostatin sequence by PCR
CC using primers ADN00610 and ADN00613.

XX Sequence 18 AA;

Query Match 100.0%; Score 85; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
| | | | | | | | | | | | | | | | | |
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 5

ADOS5472

ID ADO55472 standard; peptide; 18 AA.

XX AC ADO55472;

XX 15-JUL-2004 (first entry)

XX Murine E3/19K N-terminal peptide.

XX nitrogen monoxide; NO; signal cascade modulator;

XX human endostatin regulation; neuroprotective; neurotropic;

XX cerebroprotective; vulnerary; cerebroprotective; protozoacide;

XX cytostatic; degenerative disease; infection; CNS; Alzheimer's disease;

XX cranial-cerebral trauma; cerebral malaria; tumour; glioblastoma;

XX astroblastoma; oligodendroglioma.

XX Mus sp.

XX DE10240735-A1.

XX 18-MAR-2004.

XX 29-AUG-2002; 2002DE-01040735.

XX 29-AUG-2002; 2002DE-01040735.

XX (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.

XX Deininger MH;

XX WPI; 2004-258561/25.

XX Regulating human endostatin expression, e.g. for treating CNS disorders
or tumors, using nitrogen monoxide signal cascade modulators.

XX Example; Page 8; 18pp; German.

XX This invention describes the use of nitrogen monoxide (NO) signal cascade
CC modulators in the production of medicaments for regulating human
CC endostatin expression. The modulators described are NO synthase
CC inhibitors, especially aminoguanidine, N(G)-nitro-L-arginine methyl ester
CC (L-NAME), S-methyl-isothiourea, N(G)-monomethyl-L-arginine acetate (L-
CC NNMA), N(gamma)-nitro-L-arginine, S-2-aminoethyl-isothiourea, S-ethyl-
CC isothiourea, 2-amino-4-methyl-pyridine or L-N(6)-(1-iminoethyl)-lysine.

CC The products of the invention have neuroprotective, neurotropic,

CC cerebroprotective, vulnerary, cerebroprotective, protozoacide and

CC cytostatic activity. Where the modulators are NO synthase inhibitors or

CC NO scavenging reagents, they are specifically used for treating

CC degenerative diseases and/or infections of the CNS, especially

CC Alzheimer's disease, cranial-cerebral trauma or cerebral malaria. Where

CC the signal cascade modulators are NO donors or NO synthase stimulants,

CC they are specifically used for treating tumors, especially

CC glioblastomas, astroblastomas or oligodendrogliomas. The signal cascade

CC modulators are effective in regulating the levels of endostatin (a 20 kD

CC C-terminal fragment of collagen XVIII, causing inhibition of angiogenesis

CC and tumour growth), without the need for external administration of

CC endostatin itself.

XX Sequence 18 AA;

Query Match 100.0%; Score 85; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
| | | | | | | | | | | | | | | | | |

Db 1 MRYMILGLLALAAVCSAA 18

RESULT 6

ADO43914

ID ADO43914 standard; peptide; 18 AA.

XX

AC ADO43914;

DT 15-JUL-2004 (first entry)

DE Amino acid sequence of the E3/19K signal peptide.

KW retina; endostatin; vascular endothelial growth factor receptor;

KW pigment epithelium-derived factor; angiostatin; plasminogen fragment;

KW rod-derived cone viability factor; antiangiogenic antithrombin;

KW cartilage-derived inhibitor; CD59 complement fragment;

KW fibronectin fragment; Gro-beta; heparinase; chorionic gonadotropin;

KW interferon; interferon inducible protein; IP-10; interleukin-12;

KW kringle 5; metalloproteinase inhibitor; placental ribonuclease inhibitor;

KW plasminogen activator inhibitor; platelet factor-4; PF4; prolactin;

KW proliferin-related protein; PRP; thrombospondin-1; TSP-1;

KW transforming growth factor-beta; TGF-beta; vasculostatin; vasostatin;

KW calreticulin; retinal disorder; retinal detachment; diabetic retinopathy;

KW retinal neovascularization; choroidal neovascularization; retinal edema.

XX unidentified adenovirus.

OS Synthetic.

OS WO2004028635-A1.

XX

PN 08-APR-2004.

XX

PD 26-SEP-2003; 2003WO-EP010725.

PF

XX 27-SEP-2002; 2002US-0414048P.

PR

XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS PHARMA GMBH.

XX

PI Campochiaro PA, Kaleko M;

XX

XX WPI; 2004-305131/28.

DR

XX Delivering a protein to the retina of a subject for treating retinal disorders, e.g., retinal detachment, retinal edema or diabetic retinopathy by periorcularly injecting a viral vector comprising a protein -encoding nucleic acid.

XX

PS Example 1; Page 11; 47pp; English.

XX

CC The specification describes a method for delivering a protein to the retina of a subject. The method comprises periorcularly injecting a viral vector comprising a nucleic acid encoding endostatin. Alternatively, the viral vector may encode soluble vascular endothelial growth factor receptor, pigment epithelium-derived factor, angiostatin (plasminogen fragment), rod-derived cone viability factor, antiangiogenic antithrombin HI, cartilage-derived inhibitor (GPI), CD59 complement fragment, fibronectin fragment, Gro-beta, a heparinase, human chorionic gonadotropin (hCG), an interferon, interferon inducible protein (IP-10), interleukin-12, kringle 5 (plasminogen fragment), metalloproteinase inhibitors (TBVPS), placental ribonuclease inhibitor, plasminogen activator inhibitor, platelet factor-4 (PF4), prolactin 16kD fragment, proliferin-related protein (PRP), thrombospondin-1 (TSP-1), transforming growth factor-beta (TGF-beta), vasculostatin or vasostatin (calreticulin fragment). The method is useful in delivering a protein to the retina of a subject for treatment of retinal disorders, e.g., retinal detachment, diabetic retinopathy, retinal neovascularization, choroidal neovascularization or retinal edema. The present signal peptide was attached to murine endostatin, and used to construct viral vectors for use in the method of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 85; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18

Db 1 MRYMILGLLALAAVCSAA 18

RESULT 7

AAR63153

ID AAR63153 standard; peptide; 27 AA.

XX

AC AAR63153;

DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 19-MAY-1995 (first entry)

XX

DE PLA tumour peptide and signal peptide.

XX

KW Signal peptide; immunogen; chimeric protein; tumour peptide; vaccine;

KW bacterial peptide; parasitic peptide; autoimmune disease; immunisation;

KW T-cell response; virus; cancer; viral infection; bacterial infection;

KW parasitic infection; mammal.

XX

OS Homo sapiens.

OS Human adenovirus type 5.

XX

PN WO9421680-A1.

XX

PD 29-SEP-1994.

XX

PF 17-MAR-1994; 94WO-US002897.

XX

PR 17-MAR-1993; 93US-00032902.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

XX Restifo NP, Rosenberg SA, Bennink JR, Bacik I, Yewdell JW;

XX

XX WPI; 1994-316942/39.

DR

XX Chimeric proteins comprising endo-plasmic reticulum signal sequence - for use in vaccines against bacteria, viruses and parasites and for treating cancer and auto-immune disease.

XX

PS Disclosure; Page 9; 51pp; English.

XX

CC This sequence represents an immunogenic chimeric protein comprising the PLA peptide derived from P815 mastocytoma cells and the adenovirus type 5 E3/19 K gene product signal peptide. This sequence represents the immunogenic chimeric protein of the invention. Various signal peptides may be linked to at least one other peptide selected from tumour peptides such as this, bacterial peptides, parasitic peptides and autoimmune disease peptides. Nucleic acids encoding the chimeric proteins may be used for immunisation, eliciting a T-cell response against the tumour peptide or viral peptide they encode. The proteins may be used in vaccines and in the treatment of cancer, viral infection, bacterial infection, parasitic infection or autoimmune disease in a mammal. CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 27 AA;

Query Match 100.0%; Score 85; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 3.7e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18

Db 1 MRYMILGLLALAAVCSAA 18

RESULT 8
 AAY05400
 ID AAY05400 standard; peptide; 27 AA.
 AC AAY05400;
 XX
 DT 01-JUL-1999 (first entry)
 XX
 DE T-cell Beta-gal epitope with leader peptide.
 XX
 KW T-cell; beta-galactosidase epitope; beta-gal; tumour growth reduction;
 KW recombinant influenza virus; tumour-associated antigen; vaccine;
 KW tumour formation prevention.
 XX
 OS Unidentified.
 XX
 PN WO9848834-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 30-APR-1998; 98WO-US008929.
 XX
 PR 30-APR-1997; 97US-0045176P.
 XX
 PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 PA (USSH) US NAT INST OF HEALTH.
 XX
 XX Garcia-Sastre A, Palese P, Rosenberg SA, Restifo NP;
 PI WPI; 1999-024033/02.
 DR
 XX Recombinant influenza viruses containing tumour-associated antigen
 PT sequence - inserted into a structural gene, is useful for immunising
 PT patients to reduce or prevent tumours.
 XX
 PS Example; Fig 1; 36pp; English.
 XX
 CC This sequence represents a T-cell beta-galactosidase (beta-gal) epitope
 CC with a leader peptide. The invention relates to a recombinant influenza
 CC virus genome which contains a region encoding a tumour-associated antigen
 CC (such as this sequence). The recombinant virus is used in immunogenic
 CC formulations or vaccines for immunising tumour-bearing or tumour-free
 CC patients in order to reduce tumour growth or prevent tumour formation
 CC respectively
 CC
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 85; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRYMILGLLALAAVCSAA 18
 |||||
 Db 1 MRYMILGLLALAAVCSAA 18
 |||||
 RESULT 9
 AAW81051
 ID AAW81051 standard; peptide; 28 AA.
 AC AAW81051;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Signal peptide-cytotoxic T cell epitope fusion.
 XX
 KW MG50; melanoma gene-50; melanoma associated antigen; human; cancer;
 KW lung cancer; rhabdomyosarcoma; diagnosis; therapy; vaccine;
 KW cytotoxic T cell epitope; signal peptide.
 XX
 OS Synthetic.

OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18 /note= "signal peptide"
 FT Peptide 19..28
 FT Peptide /note= "cytotoxic T cell epitope"
 XX
 PN WO9855133-A1.
 XX
 PD 10-DEC-1998.
 XX
 PF 04-JUN-1998; 98WO-US011533.
 XX
 PR 06-JUN-1997; 97US-00870941.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX
 PI Mitchell MS, Deans RJ, Minev BR, Kan-Mitchell J;
 XX WPI; 1999-080820/07.
 DR
 XX New MG50 melanoma associated antigen fragments - used to develop products
 PT for the detection, treatment and prevention of MG50-expressing cancers,
 PT e.g. melanoma, lung cancer or rhabdomyosarcoma.
 XX
 PS Claim 12; Page 58; 79pp; English.
 XX
 CC This peptide comprises a claimed cytotoxic T cell epitope composed of a
 CC signal peptide and a T cell epitope (see AAW81032) derived from the human
 CC MG50 melanoma associated antigen (see AAW81030). The signal peptide can
 CC facilitate presentation of the epitope as a complex with an MHC molecule
 CC at the surface of an antigen presenting cell (APC). The invention
 CC provides additional T cell epitopes (see AAW81031-45) from MG50, and APCs
 CC that can express an MG50 T cell epitope complexed with an MHC molecule on
 CC their surfaces, and which can be administered to a patient having a
 CC cancer that contains MG50-expressing cells in order to stimulate an
 CC active immune response. MG50 vaccines comprising an MG50 polypeptide, a T
 CC cell epitope optionally attached to a signal peptide, an anti-idiotypic
 CC antibody or a nucleic acid molecule encoding an MG50 polypeptide or T
 CC cell epitope can be administered for preventative or therapeutic
 CC purposes. The products and methods are used for the detection, treatment
 CC and prevention of e.g. melanoma, lung cancer and rhabdomyosarcoma
 XX
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 85; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRYMILGLLALAAVCSAA 18
 |||||
 Db 1 MRYMILGLLALAAVCSAA 18
 |||||
 RESULT 10
 ABU87179
 ID ABU87179 standard; peptide; 48 AA.
 XX
 AC ABU87179;
 XX
 DT 03-JUL-2003 (first entry)
 XX
 DE Expression vector pCDNaggi expressed protein.
 XX
 KW Carbohydrate antigen; mimotype; vaccine; infection; tumour; pathogen;
 KW cytostatic; antibacterial; antigen; E3 leader sequence; HIV;
 KW T helper cell epitope.
 XX
 OS Human immunodeficiency virus 1.
 OS unidentified adenovirus.

OS Synthetic.
 XX US2003017497-A1.
 XX PD 23-JAN-2003.
 XX PF 28-JUN-2001; 2001US-00894594.
 XX PR 04-FEB-1998; 98US-0073690P.
 XX PR 04-FEB-1999; 99WO-US002405.
 XX PR 28-JUN-2000; 2000US-0214517P.
 XX PR 07-NOV-2000; 2000US-00601558.
 XX (KIEB/) KIEBER-EMMONS T.
 PA (WEIN/) WEINER D B.
 PA (MONZ/) MONZAVI-KARBASSI B.
 XX Kieber-Emmons T, Weiner DB, Monzavi-Karbassi B;
 XX WPI; 2003-401670/38.
 XX Preparing a recombinant antibody or peptide that mimics an antigenic
 PT carbohydrate, for generating an immune response against a pathogen,
 PT comprises identifying a peptide sequence that is cross reactive with an
 PT antigenic carbohydrate.
 XX Example 9; Fig 11; 75pp; English.
 XX The invention relates to preparing a recombinant antibody or a peptide
 CC that mimics an antigenic carbohydrate comprising identifying a peptide
 CC sequence that is immunogenically cross reactive with an antigenic
 CC carbohydrate, and synthesising a recombinant antibody comprising the
 CC peptide sequence or a peptide comprising at least two repeating units of
 CC the peptide sequence. Also included are a method of generating an immune
 CC response against a pathogen or tumour cell in an individual (comprising
 CC administering to the individual the carbohydrate antigen peptide mimotope
 CC vaccine comprising a nucleic acid sequence that encodes then peptides of
 CC the invention), a method of enhancing binding of anti-antigenic
 CC carbohydrate antibodies to the antigenic carbohydrate in an individual
 CC (comprising administering to the individual anti-antigenic carbohydrate
 CC antibodies and a peptide comprising 1-3 repeat units of a peptide
 CC sequence that mimics an antigenic carbohydrate), a method of inhibiting
 CC binding of a ligand to a receptor that is an antigenic carbohydrate using
 CC the peptides/antibodies of the invention and a method of identifying
 CC peptide sequences that can induce an immune response against two or more
 CC different pathogens (comprising identifying a peptide sequence that is
 CC immunogenically cross reactive with an antigenic carbohydrate, which is
 CC associated with a pathogen, administering a peptide comprising the
 CC peptide sequence to an animal to induce an immune response and analysing
 CC the immune response to identify two or more pathogens against which the
 CC immune response cross reacts. The peptides, antibodies and methods are
 CC useful for generating a prophylactic or therapeutic immune response
 CC against a tumour cell or a pathogen in an individual. The peptides are
 CC useful as immunogenic agents, vaccines, adjuvants, enhancers of antibody
 CC binding, or inhibitors of receptor/ligand binding. The methods are also
 CC useful for enhancing binding of anti-antigenic carbohydrate antibodies to
 CC the antigenic carbohydrate in an individual, inhibiting binding of a
 CC ligand to a receptor that is an antigenic carbohydrate, or identifying
 CC peptide sequences that can induce an immune response. The mimotope
 CC peptides may be expressed from a vector as a fusion protein with an
 CC adenovirus E3 leader sequence and an HIV (human immunodeficiency virus) T
 CC helper cell epitope. The present sequence is an example of a fusion
 CC protein detailed above (leader sequence-T helper epitope-mimotope
 CC peptide)
 XX Sequence 48 AA;
 SQ Query Match 100.0%; Score 85; DB 6; Length 48;
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRYMILGLLALAAVCSAA 18

DB 1 MRYMILGLLALAAVCSAA 18
 RESULT 11
 ABU87178
 ID ABU87178 standard; peptide; 56 AA.
 XX AC ABU87178;
 XX DT 03-JUL-2003 (first entry)
 XX DE Carbohydrate antigen peptide mimotope #64.
 XX Carbohydrate antigen; mimotope; vaccine; infection; tumour; pathogen;
 KW cytostatic; antibacterial; antigen.
 XX Synthetic.
 XX OS
 XX US2003017497-A1.
 XX PD 23-JAN-2003.
 XX PF 28-JUN-2001; 2001US-00894594.
 XX PR 04-FEB-1998; 98US-0073690P.
 XX PR 04-FEB-1999; 99WO-US002405.
 XX PR 28-JUN-2000; 2000US-0214517P.
 XX PR 07-NOV-2000; 2000US-00601558.
 XX (KIEB/) KIEBER-EMMONS T.
 PA (WEIN/) WEINER D B.
 PA (MONZ/) MONZAVI-KARBASSI B.
 XX Kieber-Emmons T, Weiner DB, Monzavi-Karbassi B;
 XX WPI; 2003-401670/38.
 XX Preparing a recombinant antibody or peptide that mimics an antigenic
 PT carbohydrate, for generating an immune response against a pathogen,
 PT comprises identifying a peptide sequence that is cross reactive with an
 PT antigenic carbohydrate.
 XX Example 1; Page 12; 75pp; English.
 XX The invention relates to preparing a recombinant antibody or a peptide
 CC that mimics an antigenic carbohydrate comprising identifying a peptide
 CC sequence that is immunogenically cross reactive with an antigenic
 CC carbohydrate, and synthesising a recombinant antibody comprising the
 CC peptide sequence or a peptide comprising at least two repeating units of
 CC the peptide sequence. Also included are a method of generating an immune
 CC response against a pathogen or tumour cell in an individual (comprising
 CC administering to the individual the carbohydrate antigen peptide mimotope
 CC vaccine comprising a nucleic acid sequence that encodes then peptides of
 CC the invention), a method of enhancing binding of anti-antigenic
 CC carbohydrate antibodies to the antigenic carbohydrate in an individual
 CC (comprising administering to the individual anti-antigenic carbohydrate
 CC antibodies and a peptide comprising 1-3 repeat units of a peptide
 CC sequence that mimics an antigenic carbohydrate), a method of inhibiting
 CC binding of a ligand to a receptor that is an antigenic carbohydrate using
 CC the peptides/antibodies of the invention and a method of identifying
 CC peptide sequences that can induce an immune response against two or more
 CC different pathogens (comprising identifying a peptide sequence that is
 CC immunogenically cross reactive with an antigenic carbohydrate, which is
 CC associated with a pathogen, administering a peptide comprising the
 CC peptide sequence to an animal to induce an immune response and analysing
 CC the immune response to identify two or more pathogens against which the
 CC immune response cross reacts. The peptides, antibodies and methods are
 CC useful for generating a prophylactic or therapeutic immune response
 CC against a tumour cell or a pathogen in an individual. The peptides are
 CC useful as immunogenic agents, vaccines, adjuvants, enhancers of antibody
 CC binding, or inhibitors of receptor/ligand binding. The methods are also
 CC useful for enhancing binding of anti-antigenic carbohydrate antibodies to
 CC the antigenic carbohydrate in an individual, inhibiting binding of a
 CC ligand to a receptor that is an antigenic carbohydrate, or identifying
 CC peptide sequences that can induce an immune response. The mimotope
 CC peptides may be expressed from a vector as a fusion protein with an
 CC adenovirus E3 leader sequence and an HIV (human immunodeficiency virus) T
 CC helper cell epitope. The present sequence is an example of a fusion
 CC protein detailed above (leader sequence-T helper epitope-mimotope
 CC peptide)
 XX Sequence 48 AA;
 SQ Query Match 100.0%; Score 85; DB 6; Length 48;
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRYMILGLLALAAVCSAA 18

CC useful for enhancing binding of anti-antigenic carbohydrate antibodies to
 CC the antigenic carbohydrate in an individual, inhibiting binding of a
 CC ligand to a receptor that is an antigenic carbohydrate, or identifying
 CC peptide sequences that can induce an immune response. The present
 CC sequence is a carbohydrate antigen minotype peptide of the invention
 XX
 SQ Sequence 56 AA;

Query Match 100.0%; Score 85; DB 6; Length 56;
 Best Local Similarity 100.0%; Pred. No. 8.2e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
 |||||
 Db 1 MRYMILGLLALAAVCSAA 18

RESULT 12
 AAY4964
 ID AAY4964 standard; protein; 90 AA.

XX AC AAY4964;

DT 12-SEP-2003 (revised)
 DT 23-MAY-2000 (first entry)

XX KDEL receptor inhibitor protein-7.

XX KDEL receptor inhibitor; heat shock protein; immune response;
 KW oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia;
 KW melanoma; carcinoma; glioblastoma; astrocytoma; oncogene;
 KW infectious disease; allergy; autoimmune disease.

XX unidentified adenovirus; E3.
 OS Homo sapiens.
 OS Camelus sp.
 OS Chimeric.

XX Key Location/Qualifiers
 FT Peptide 1..20
 /note= "Derived from adenovirus E3"
 FT Domain 30..56
 /note= "Human phospholamban pentamerisation domain"
 FT Domain 57..80
 /note= "Camel IgG linker domain"

XX WO200006729-A1.

XX 10-FEB-2000.

XX 28-JUL-1999; 99WO-US017147.

XX 29-JUL-1998; 98US-00124671.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Rothman JE, Mayhew M, Hoe MH;

XX WPI; 2000-195296/17.

XX N-PSDB; AAZ50498.

XX Inhibitors of the KDEL receptor which comprises an oligomerization domain
 PT useful for promoting secretion of proteins which are normally retained
 PT within the cell.

XX Disclosure; Fig 7; 87pp; English.

XX The patent discloses the use of KDEL receptor inhibitor to promote
 CC secretion of proteins that are normally retained within the cell such as
 CC heat shock proteins by inhibiting KDEL receptor-mediated return of
 CC protein complexes to endoplasmic reticulum. This makes the secreted heat
 CC shock proteins more accessible to the immune system and improves immune
 CC response to a target antigen. The inhibitor protein comprises several

CC subunits where each subunit comprises an oligomerisation domain and has
 CC at its carboxy terminus a region which binds to a KDEL receptor. The
 CC target antigen may be associated with diseases including neoplasia such
 CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and
 CC astrocytoma, with defective tumour suppressor genes, oncogenes,
 CC infectious diseases, allergy or autoimmune diseases. The present sequence
 CC is KDEL receptor inhibitor comprising regions encoding a cleavable signal
 CC peptide; the oligomerisation domain of human phospholamban (PLB)
 CC pentamerisation domain; a camel IgG linker domain and the carboxy-
 CC terminal sequence KDEL. The subsequence GDCC is an alteration of rat
 CC cartilage oligomeric matrix protein which provides increased stability
 CC via disulphide bonds. (Updated on 12-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 90 AA;

Query Match 100.0%; Score 85; DB 3; Length 90;

Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
 |||||
 Db 1 MRYMILGLLALAAVCSAA 18

RESULT 13

AAY4963

ID AAY4963 standard; protein; 109 AA.

XX AC AAY4963;

XX 12-SEP-2003 (revised)

DT 23-MAY-2000 (first entry)

XX KDEL receptor inhibitor protein-6.

XX KDEL receptor inhibitor; heat shock protein; immune response;
 KW oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia;
 KW melanoma; carcinoma; glioblastoma; astrocytoma; oncogene;
 KW infectious disease; allergy; autoimmune disease.

XX unidentified adenovirus; E3.

OS Homo sapiens.

OS Camelus sp.

OS Chimeric.

XX Key Location/Qualifiers

FT Peptide 1..20
 /label= Signal peptide

FT Domain 30..75
 /note= "Derived from adenovirus E3"

FT Domain 76..99
 /note= "Human COMP pentamerisation domain"

FT Domain 76..99
 /note= "Camel IgG linker domain"

XX WO200006729-A1.

XX 10-FEB-2000.

XX 28-JUL-1999; 99WO-US017147.

XX 29-JUL-1998; 98US-00124671.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Rothman JE, Mayhew M, Hoe MH;

XX WPI; 2000-195296/17.

XX N-PSDB; AAZ50497.

XX Inhibitors of the KDEL receptor which comprises an oligomerization domain
 PT useful for promoting secretion of proteins which are normally retained
 PT within the cell.

PS Disclosure; Fig 6; 87pp; English.

XX The patent discloses the use of KDEL receptor inhibitor to promote

CC secretion of proteins that are normally retained within the cell such as

CC heat shock proteins by inhibiting KDEL receptor-mediated return of

CC protein complexes to endoplasmic reticulum. This makes the secreted heat

CC shock proteins more accessible to the immune system and improves immune

CC response to a target antigen. The inhibitor protein comprises several

CC subunits where each subunit comprises an oligomerisation domain and has

CC at its carboxy terminus a region which binds to a KDEL receptor. The

CC target antigen may be associated with diseases including neoplasia such

CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and

CC astromyoma, with defective tumour suppressor genes, oncogenes,

CC infectious diseases, allergy or autoimmune diseases. The present sequence

CC is KDEL receptor inhibitor comprising regions encoding a cleavable signal

CC peptide; the oligomerisation domain of human cartilage oligomeric matrix

CC protein (COMP) pentamerisation domain; a camel IgG linker domain and the

CC carboxy-terminal sequence KDEL. The subsequence GDCC is an alteration of

CC rat COMP which provides increased stability via disulphide bonds.

CC (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 109 AA;

Query Match 100.0%; Score 85; DB 3; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18

DB 1 MRYMILGLLALAAVCSAA 18

RESULT 14

AAV44965

ID AAY44965 standard; protein; 109 AA.

XX AAY44965;

AC AAY44965;

XX 12-SEP-2003 (revised)

DT 23-MAY-2000 (first entry)

DE KDEL receptor inhibitor protein-8.

XX KDEL receptor inhibitor; heat shock protein; immune response;

KW oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia;

KW melanoma; carcinoma; glioblastoma; astromyoma; oncogene;

KW infectious disease; allergy; autoimmune disease.

XX unidentified adenovirus; E3.

OS Homo sapiens.

OS Camelus sp.

OS Chimeric.

XX Key Location/Qualifiers

FT Peptide 1..20

FT /label= Signal peptide

FT /note= "Derived from adenovirus E3"

FT Domain 30..75

FT /note= "Human TSP 3 trimerisation domain"

FT Domain 76..99

FT /note= "Camel IgG linker domain"

XX WO200006729-A1.

PN 10-FEB-2000.

XX 28-JUL-1999; 99WO-US017147.

XX 29-JUL-1998; 98US-00124671.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Rothman JE, Mayhew M, Hoe MH;

PI

XX WPI; 2000-195296/17.

DR N-PSDB; AAZ50499.

XX Inhibitors of the KDEL receptor which comprises an oligomerization domain

PT useful for promoting secretion of proteins which are normally retained

PT within the cell.

XX Disclosure; Fig 8; 87pp; English.

XX The patent discloses the use of KDEL receptor inhibitor to promote

CC secretion of proteins that are normally retained within the cell such as

CC heat shock proteins by inhibiting KDEL receptor-mediated return of

CC protein complexes to endoplasmic reticulum. This makes the secreted heat

CC shock proteins more accessible to the immune system and improves immune

CC response to a target antigen. The inhibitor protein comprises several

CC subunits where each subunit comprises an oligomerisation domain and has

CC at its carboxy terminus a region which binds to a KDEL receptor. The

CC target antigen may be associated with diseases including neoplasia such

CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and

CC astromyoma, with defective tumour suppressor genes, oncogenes,

CC infectious diseases, allergy or autoimmune diseases. The present sequence

CC is KDEL receptor inhibitor comprising regions encoding a cleavable signal

CC peptide; the oligomerisation domain of human thrombospondin 3 (TSP3)

CC trimerisation domain; a camel IgG linker domain and the carboxy-terminal

CC sequence KDEL. The subsequence GDCC is an alteration of rat cartilage

CC oligomeric matrix protein which provides increased stability via

CC disulphide bonds. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 109 AA;

Query Match 100.0%; Score 85; DB 3; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18

DB 1 MRYMILGLLALAAVCSAA 18

RESULT 15

AAV44966

ID AAY44966 standard; protein; 109 AA.

XX AAY44966;

AC AAY44966;

XX 12-SEP-2003 (revised)

DT 23-MAY-2000 (first entry)

DE KDEL receptor inhibitor protein-9.

XX KDEL receptor inhibitor; heat shock protein; immune response;

KW oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia;

KW melanoma; carcinoma; glioblastoma; astromyoma; oncogene;

KW infectious disease; allergy; autoimmune disease.

XX unidentified adenovirus; E3.

OS Homo sapiens.

OS Camelus sp.

OS Chimeric.

XX Key Location/Qualifiers

FT Peptide 1..20

FT /label= Signal peptide

FT /note= "Derived from adenovirus E3"

FT Domain 30..75

FT /note= "Human TSP4 trimerisation domain"

FT Domain 76..99

FT /note= "Camel IgG linker domain"

XX WO200006729-A1.

PN 10-FEB-2000.

XX 28-JUL-1999; 99WO-US017147.
PF
XX 29-JUL-1998; 98US-00124671.
PR
XX (SLOK) SLOAN KETTERING INST CANCER RES.
PA
XX Rothman JE, Mayhew M, Hoe MH;
PI
XX WPI; 2000-195296/17.
DR N-PSDB; AAZ50500.
XX
PT Inhibitors of the KDEL receptor which comprises an oligomerization domain
PT useful for promoting secretion of proteins which are normally retained
PT within the cell.
PT
XX
XX Disclosure; Fig 9; 87pp; English.
XX
XX The patent discloses the use of KDEL receptor inhibitor to promote
CC secretion of proteins that are normally retained within the cell such as
CC heat shock proteins by inhibiting KDEL receptor-mediated return of
CC protein complexes to endoplasmic reticulum. This makes the secreted heat
CC shock proteins more accessible to the immune system and improves immune
CC response to a target antigen. The inhibitor protein comprises several
CC subunits where each subunit comprises an oligomerisation domain and has
CC at its carboxy terminus a region which binds to a KDEL receptor. The
CC target antigen may be associated with diseases including neoplasia such
CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and
CC astrocytoma, with defective tumour suppressor genes, oncogenes,
CC infectious diseases, allergy or autoimmune diseases. The present sequence
CC is KDEL receptor inhibitor comprising regions encoding a cleavable signal
CC peptide; the oligomerisation domain of human thrombospondin 4 (TSP4)
CC trimerisation domain; a camel IgG linker domain and the carboxy-terminal
CC sequence KDEL. The subsequence GDCC is an alteration of rat cartilage
CC oligomeric matrix protein which provides increased stability via
CC disulphide bonds. (Updated on 12-SEP-2003 to standardise OS field)
XX
XX Sequence 109 AA;

Query Match 100.0%; Score 85; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRYMILGLLALAAVCSAA 18
DB 1 MRYMILGLLALAAVCSAA 18

Search completed: January 11, 2006, 00:08:16
Job time : 77 secs

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OM protein - protein search, using sw model

Run on: January 11, 2006, 00:05:17 ; Search time 16 Seconds
(without alignments)
108.244 Million cell updates/sec

Title: US-10-031-008-7
Perfect score: 85
Sequence: 1 MRYMILGLLALAAVCSSA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: Pir1: *
2: Pir2: *
3: Pir3: *
4: Pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	159	1 Q6ADE	early E3 18.5K gly
2	47	55.3	596	2 T19740	hypothetical prote
3	46	54.1	131	2 D83173	hypothetical prote
4	46	54.1	5175	2 T20992	hypothetical prote
5	46	54.1	5198	2 T43290	hemocentin precurs
6	45	52.9	160	1 ERADA5	early E3 18.5K gly
7	45	52.9	3390	1 GNWVD3	genome polypeptide
8	44	51.8	152	2 T48227	hypothetical prote
9	44	51.8	255	2 E72522	hypothetical prote
10	44	51.8	334	2 D87575	hypothetical prote
11	44	51.8	372	2 AB0276	probable membrane
12	44	51.8	742	2 A49340	alcohol dehydrogen
13	44	51.8	742	2 JS0326	hypothetical prote
14	43.5	51.2	152	2 G83476	hypothetical prote
15	43	50.6	64	2 T25247	osteocalcin precur
16	43	50.6	100	1 GEB0	hypothetical prote
17	42	49.4	100	1 GEHU	hypothetical prote
18	42	49.4	221	2 A70543	ferric enterobacti
19	42	49.4	334	2 S16296	ferric enterobacti
20	42	49.4	334	2 A85558	ferric enterobacti
21	42	49.4	334	2 E90707	ferric enterobacti
22	42	49.4	335	2 AB0575	manganese peroxida
23	42	49.4	380	2 JC2579	probable MFS trans
24	42	49.4	408	2 B83333	heat shock protein
25	42	49.4	417	1 A40968	heat shock protein
26	42	49.4	417	1 A42843	heat shock protein
27	42	49.4	417	1 S20608	calcium channel pr
28	42	49.4	2223	2 A47447	MG277 homolog Fl1
29	41.5	48.8	887	2 S73768	

30	41	48.2	63	2 H84265	hypothetical prote
31	41	48.2	109	2 A64916	probable membrane
32	41	48.2	109	2 A99917	probable chaperone
33	41	48.2	109	2 F85765	probable chaperone
34	41	48.2	109	2 D75604	hypothetical prote
35	41	48.2	132	2 A10543	probable secreted
36	41	48.2	149	2 S6501	yjgY protein - Esc
37	41	48.2	207	2 S6501	secreted protein, Esc
38	41	48.2	207	2 A80632	hypothetical prote
39	41	48.2	324	2 S75026	iron ABC transport
40	41	48.2	324	2 F75631	Na/taurocholate co
41	41	48.2	349	2 I55601	hypothetical prote
42	41	48.2	396	2 T45033	probable large sec
43	41	48.2	613	2 T36922	homeotic protein B
44	41	48.2	640	2 A41726	homeotic protein B
45	41	48.2	642	2 S27806	methyl-accepting c
			781	2 A13014	

ALIGNMENTS

RESULT 1

Q6ADE
early E3 18.5K glycoprotein - human adenovirus 2
C:Species: Mastadenovirus h2 (human adenovirus 2)
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1980 #sequence_revision 08-Oct-1981 #text_change 09-Jul-2004
C:Accession: A03821
R:Herisse, J.; Courtois, G.; Galibert, F.
Nucleic Acids Res. 8, 2173-2192, 1980
A:Title: Nucleotide sequence of the EcoRI D fragment of adenovirus 2 genome.
A:Reference number: A93702; MUID:81053687; PMID:6253880
A:Accession: A03821
A:Molecule type: DNA
A:Residues: 1-159 <HER>
A:Cross-references: UNIPROT:P03251; UNIPARC:UPI00000000D85
C:Superfamily: adenovirus early E3 18.5K glycoprotein
C:Keywords: early protein; glycoprotein; transmembrane protein
F:29,78/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 85; DB 1; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSSA 18
DB 1 MRYMILGLLALAAVCSSA 18
|||||

RESULT 2

T19740
hypothetical protein C35A5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19740
R:Matthews, P.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z19172
A:Accession: T19740
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-596 <WIL>
A:Cross-references: UNIPROT:Q18472; UNIPARC:UPI000007F46A; EMBL:Z71185; PIDN:CAA34905.1
A:Experimental source: clone C35A5
C:Genetics:
A:Gene: CRSP:C35A5.3
A:Map position: 5
A:Introns: 24/1; 67/3; 90/2; 123/2; 181/3; 257/3; 371/3; 441/2; 468/2; 505/2

Query Match 55.3%; Score 47; DB 2; Length 596;
Best Local Similarity 64.7%; Pred. No. 16;
Matches 11; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 RYMIL--GLLAAVCS 16
||:|||||
Db 141 RYLILIVGFLCLASVCS 157

RESULT 3
D83173
hypoetical protein PA3788 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: D83173
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83173
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-131 <STO>
A:Cross-references: UNIPROT:Q9HKK7; UNIPARC:UPI00000C5B13; GB:AE004797; GB:AE004091; NID:10984043
C:Genetics:
A:Gene: PA3788

Query Match 54.1%; Score 46; DB 2; Length 131;
Best Local Similarity 56.2%; Pred. No. 7.3;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYMILGLLAAVCSA 17
||:|||||
Db 70 RYLVLGLLAAVIAVS 85

RESULT 4
T20992
hypoetical protein F15G9.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20992, T24733
R:Sulston, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20992
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-5175 <WIL>
A:Cross-references: UNIPROT:Q8IOL3; UNIPARC:UPI00001101B6; EMBL:Z47068; PIDN:CAA87335.1;
A:Experimental source: clone F15G9
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24733
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-5175 <WIL>
A:Cross-references: UNIPROT:Q8IOL3; UNIPARC:UPI00001101B6; EMBL:Z47068; PIDN:CAA87335.1;
A:Experimental source: clone F15G9

Query Match 54.1%; Score 46; DB 2; Length 5175;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 YMILGLLAAVCSA 17
||:|||||
Db 9 YGVILGLLAAVTCSS 23

RESULT 5
T43290

hemocentin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43290; T20993; T24734
R:Voegel, B.E.; Hedgecock, E.M.

A:Description: Hemocentin is required for hemidesmosome mediated cell adhesion and germ-line development.
A:Reference number: Z22396
A:Accession: T43290
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-5198 <VOG>
A:Cross-references: UNIPROT:O76518; UNIPARC:UPI0000110172; EMBL:AF074901; PIDN:AAC26792;
R:Sulston, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20993
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-5198 <WIL>
A:Cross-references: UNIPARC:UPI0000110172; EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN000028;

A:Experimental source: Clone F15G9
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24734
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-5198 <WIL>
A:Cross-references: UNIPARC:UPI0000110172; EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN000028;

A:Experimental source: Clone F15G9
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24734
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-5198 <WIL>
A:Cross-references: UNIPARC:UPI0000110172; EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN000028;

A:Experimental source: clone T09B9
C:Genetics:
A:Gene: him-4; F15G9.4b

A:Map position: X

A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 1251/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1;

Query Match 54.1%; Score 46; DB 2; Length 5198;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 YMILGLLAAVCSA 17
||:|||||

Db 9 YGVILGLLAAVTCSS 23

RESULT 6
ERADAS

early E3 18.5K glycoprotein - human adenovirus 5

C:Species: Mastadenovirus h5 (human adenovirus 5)

A:Note: host Homo sapiens (man)

C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004

C:Accession: A03822; A22515

R:Cladaras, C.; Wold, W.S.M.

Virology 140, 28-43, 1985

A:Title: DNA sequence of the early E3 transcription unit of adenovirus 5.

A:Reference number: A94335; MUID:85092388; PMID:2981456

A:Accession: A03822

A:Molecule type: DNA

A:Residues: 1-160 <CLA>

A:Cross-references: UNIPROT:P04494; UNIPARC:UPI0000129AE7; GB:X03002; NID:g58503; PIDN:

R:Wold, W.S.M.; Cladaras, C.; Deutscher, S.L.; Kapoor, Q.S.

J. Biol. Chem. 260, 2424-2431, 1985

A:Title: The 19-kDa glycoprotein coded by region E3 of adenovirus.

A:Reference number: A22515; MUID:85130985; PMID:3882694

A:Accession: A22515

A:Molecule type: DNA

A:Residues: 1-160 <WOL>

A;Cross-references: UNIPARC:UPI000129AE7; GB:M12406; NID:g209911; PIDN:AAA42492.1; PID:
 C;Superfamily: adenovirus early E3 18.5K glycoprotein
 C;Keywords: early protein; glycoprotein; transmembrane protein
 F;30,79/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 52.9%; Score 45; DB 1; Length 160;
 Best Local Similarity 69.2%; Pred. No. 12;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAA 13
 :|:|:|:|:|:|:
 Db 2 IRVILGLTLAS 14

RESULT 7
 GNWVD3
 genome polyprotein - dengue virus type 3
 N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS
 a; nonstructural protein NS4b; nonstructural protein NS5
 C;Species: dengue virus type 3
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
 C;Accession: A34774
 R;Osatomi, K.; Sumiyoshi, H.
 Virology 176, 643-647, 1990
 A;Title: Complete nucleotide sequence of dengue type 3 virus genome RNA.
 A;Reference number: A34774; MUID:90266483; PMID:2345967
 A;Accession: A34774
 A;Molecule type: genomic RNA
 A;Residues: 1-3390 <OSA>
 A;Cross-references: UNIPROT:P27915; UNIPARC:UPI0000131DFF; GB:M93130; NID:g323468; PIDN:
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
 F;1-114/Product: capsid protein #status predicted <CAP>
 F;46-67/Domain: transmembrane #status predicted <TM1>
 F;115-280/Product: membrane protein precursor #status predicted <MEP>
 F;115-205/Domain: nonterminal signal sequence #status predicted <SIG>
 F;206-280/Product: membrane protein #status predicted <MEM>
 F;266-280/Domain: transmembrane #status predicted <TM3>
 F;281-773/Product: envelope protein #status predicted <ENV>
 F;724-746/Domain: transmembrane #status predicted <TM4>
 F;753-771/Domain: transmembrane #status predicted <TM5>
 F;774-1184/Product: nonstructural protein NS1 #status predicted <NS1>
 F;1156-1175/Domain: transmembrane #status predicted <TM6>
 F;1185-1343/Product: nonstructural protein NS2a #status predicted <N2A>
 F;1344-1473/Product: nonstructural protein NS2b #status predicted <N2B>
 F;1474-2092/Product: nonstructural protein NS3 #status predicted <NS3>
 F;1667-1674/Region: nucleotide-binding motif A (P-loop)
 F;1754-1759/Region: nucleotide-binding motif B
 F;1758-1761/Region: DEAH motif
 F;2093-2378/Product: nonstructural protein NS4a #status predicted <N4A>
 F;2379-2490/Product: nonstructural protein NS4b #status predicted <N4B>
 F;2491-3390/Product: nonstructural protein NS5 #status predicted <NS5>
 F;183,347,433,750,903,980,1132,1188,1661,2300,2304,2386,2456,2702,2712/Binding site: car

Query Match 52.9%; Score 45; DB 1; Length 3390;
 Best Local Similarity 41.2%; Pred. No. 1.2e+02;
 Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSA 17
 :|:|:|:|:|:|:
 Db 2226 LAIVVIGLTLAAIVAA 2242

RESULT 8
 T48227
 hypothetical protein T7H20.110 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C;Accession: T48227
 R;Bavan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; New
 submitted to the Protein Sequence Database, March 2000
 A;Reference number: 224488
 A;Accession: T48227

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-152 <BEV>
 A;Cross-references: UNIPROT:Q9L2M5; UNIPARC:UPI00000A71EB; EMBL:AL162508
 A;Experimental source: cultivar Columbia; BAC clone T7H20
 C;Genetics:
 A;Map position: 5
 A;Introns: 44/2; 88/3
 A;Note: T7H20.110

Query Match 51.8%; Score 44; DB 2; Length 152;
 Best Local Similarity 64.3%; Pred. No. 16;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 ILGLLALAAVCSAA 18
 :|:|:|:|:|:|:
 Db 89 VTALLALAAACSSA 102

RESULT 9
 E72522
 hypothetical protein APE2154 - Aeropyrum pernix (strain K1)
 C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: E72522
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, Y.; Jin-no, K.; Taka;
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
 DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: E72522
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-255 <KAW>
 A;Cross-references: UNIPROT:Q9Y9Y5; UNIPARC:UPI000005E229; DBJ:AP0000063; NID:95105654;
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE2154
 C;Superfamily: conserved hypothetical protein HI0188

Query Match 51.8%; Score 44; DB 2; Length 255;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYMILGLLALAAVCS 16
 :|:|:|:|:|:|:
 Db 198 RMVLLGLLALGAVIS 212

RESULT 10
 D87575
 hypothetical protein CC2633 [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: D87575
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.I
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: D87575
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-334 <STO>
 A;Cross-references: UNIPROT:Q9A536; UNIPARC:UPI00000C77B7; GB:AB005673; NID:gl3424210;
 C;Genetics:
 A;Gene: CC2633

Query Match 51.8%; Score 44; DB 2; Length 334;
 Best Local Similarity 50.0%; Pred. No. 30;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 YMYLGLLALAAVCSAA 18
 ::|||::|
 Db 9 FVALGLMAMLAACSPA 24

RESULT 11

AB0276
 probable membrane protein YPO2266 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AB0276
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Ii, M.; Rutherford, K.; Simmonds, T.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AB0276
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-372 <KUR>
 A:Cross-references: UNIPROT:Q8ZEB5; UNIPARC:UPI00000CD8C9; GB:AL590842; PIDN:CAC91070.1;
 C:Genetics:
 A:Gene: YPO2266
 C:Superfamily: probable antibiotic resistance protein yybF

Query Match 51.8%; Score 44; DB 2; Length 372;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 MYLGLLALAAVC 15
 ::|||::|
 Db 206 LVLGLFALAAAC 217

RESULT 12

A49340
 alcohol dehydrogenase (EC 1.1.1.-) precursor - Acetobacter pasteurianus (strain NC11380)
 C:Species: Acetobacter pasteurianus
 C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Oct-2004
 C:Accession: A49340
 R:Takemura, H.; Kondo, K.; Horinouchi, S.; Beppu, T. J. Bacteriol. 175, 6857-6866, 1993
 A:Title: Induction by ethanol of alcohol dehydrogenase activity in Acetobacter pasteuria
 A:Reference number: A49340; MUID:94042848; PMID:8226628
 A:Accession: A49340
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-742 <TAK>
 A:Cross-references: UNIPROT:Q53362; UNIPARC:UPI00000BDE6D; GB:D13893; NID:g517067; PIDN:
 C:Superfamily: glucose/alcohol/Shikimate dehydrogenase
 C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 51.8%; Score 44; DB 2; Length 742;
 Best Local Similarity 47.1%; Pred. No. 54;
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 RYMILGLLALAAVCSNA 18
 |::|||::|
 Db 9 RRSLLGILAACTICAAA 25

RESULT 13

JS0326
 alcohol dehydrogenase (EC 1.1.1.-) 72K chain precursor - Acetobacter aceti
 C:Species: Acetobacter aceti
 C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 05-Oct-2004
 C:Accession: JS0326
 R:Inoue, T.; Sunagawa, M.; Mori, A.; Imai, C.; Fukuda, M.; Takagi, M.; Yano, K. J. Bacteriol. 171, 3115-3122, 1989
 A:Title: Cloning and sequencing of the gene encoding the 72-kilodalton dehydrogenase sub
 A:Reference number: JS0326; MUID:89255070; PMID:2722742
 A:Accession: JS0326

A:Molecule type: DNA
 A:Residues: 1-742 <INO>
 A:Cross-references: UNIPROT:P18278; UNIPARC:UPI000012930E; GB:D90004; GB:M26951; NID:g21
 A:Experimental source: strain K6033
 A:Note: amino terminal of mature protein is confirmed
 C:Genetics:
 A:Gene: adhI

C:Superfamily: glucose/alcohol/Shikimate dehydrogenase
 C:Keywords: alcohol metabolism; NAD; oxidoreductase
 F:1-35/Domain: signal sequence #status predicted <SIG>
 F:36-742/Product: alcohol dehydrogenase 72K dehydrogenase chain #status predicted <ADC>

Query Match 51.8%; Score 44; DB 2; Length 742;
 Best Local Similarity 47.1%; Pred. No. 54;
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 RYMILGLLALAAVCSAA 18
 |::|||::|
 Db 9 RRSLLGILAACTICAAA 25

RESULT 14

GS3476
 hypothetical protein PA1343 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: GS3476
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, K.R.; Folger, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 ; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: GS3476
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-152 <STO>
 A:Cross-references: UNIPROT:Q91401; UNIPARC:UPI00000C5326; GB:AE004564; GB:AE004091; NID:
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1343

Query Match 51.2%; Score 43.5; DB 2; Length 152;
 Best Local Similarity 68.4%; Pred. No. 19;
 Matches 13; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 MRYMLGLLLA-LAAVCSAA 18
 |||::|||::|
 Db 1 MRYLLSLLAVLAAPAWAA 19

RESULT 15

T25247
 hypothetical protein T24F1.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T25247
 R:Chui, C. submitted to the EMBL Data Library, June 1995
 A:Reference number: Z20004
 A:Accession: T25247
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-64 <WIL>
 A:Cross-references: UNIPROT:Q22746; UNIPARC:UPI0000076473; EMBL:Z49912; PIDN:CAA90139.1;
 A:Experimental source: clone T24F1
 C:Genetics:
 A:Gene: CESP:T24F1.5
 A:Map position: 2
 A:Introns: 33/1

Query Match 50.6%; Score 43; DB 2; Length 64;
 Best Local Similarity 52.9%; Pred. No. 12;

Matches	9;	Conservative	3;	Mismatches	5;	Indels	0;	Gaps	0;
Qy	1	MYMILGLLALAVCSA	17						
Db	1	MRFLILALVLFATQA	17						

Search completed: January 11, 2006, 00:10:05
Job time : 17 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: January 11, 2006, 00:04:42 ; Search time 71 Seconds
(without alignments)
178.866 Million cell updates/sec

Title: US-10-031-008-7

Perfect score: 85

Sequence: 1 MRYMILGLAALAAVCSSA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	85	100.0	159	1	E3GL_ADE02	P68978 human adeno
2	85	100.0	159	1	E3GL_ADE06	P68979 human adeno
3	85	100.0	159	2	Q910Z4_ADE02	Q910Z4 human adeno
4	85	100.0	159	2	Q779F5_ADE02	Q779F5 human adeno
5	64	75.3	160	2	O12399_ADE01	O12399 human adeno
6	54	63.5	81	2	Q75WH5_MACGS	Q75WH5 macrothelae
7	51	60.0	179	2	Q95P73_HAEIR	Q95P73 haematobia
8	51	60.0	208	2	Q7QID4_ANOGA	Q7QID4 anopheles g
9	51	60.0	234	2	Q7U6K1_SYNEX	Q7U6K1 synecococc
10	49	57.6	110	2	Q5FP07_GLUOX	Q5FP07 gluconobact
11	49	57.6	294	2	Q4USJ3_XANGP	Q4USJ3 xanthomonas
12	49	57.6	294	2	Q8PB18_XANGP	Q8PB18 xanthomonas
13	48	56.5	181	2	Q9V5Z3_DROME	Q9V5Z3 drosophila
14	48	56.5	188	2	Q9V5Z4_DROME	Q9V5Z4 drosophila
15	48	56.5	250	2	Q5UI95_DROME	Q5UI95 drosophila
16	48	56.5	490	2	Q9VLY5_DROME	Q9VLY5 drosophila
17	48	56.5	557	2	Q5NR85_ZYMO	Q5NR85 zymomonas m
18	47.5	55.9	135	1	IL5_CAVPO	Q08987 cavia porce
19	47	55.3	466	2	Q18472_CAEEL	Q18472 caenorhabdi
20	47	55.3	471	2	Q5AXY5_EMENI	Q5AXY5 aspergillus
21	47	55.3	646	2	Q6YT52_ORISA	Q6YT52 oryza sativ
22	47	55.3	647	2	Q84ZH7_ORISA	Q84ZH7 oryza sativ
23	46	54.1	131	2	Q9HKK7_PSEAB	Q9HKK7 pseudomonas
24	46	54.1	140	2	Q82PU1_STRAW	Q82PU1 streptomyce
25	46	54.1	310	2	Q8MYK4_9ASCI	Q8MYK4 boltonia vi
26	46	54.1	455	2	Q8G7U6_BIFLO	Q8G7U6 bifidobacte
27	46	54.1	523	2	Q9VLY4_DROME	Q9VLY4 drosophila
28	46	54.1	595	2	Q4V5Q2_DROME	Q4V5Q2 drosophila
29	46	54.1	1895	2	Q7RS99_GIALA	Q7RS99 giardia lam
30	46	54.1	2258	1	POL1_BAMWN	P90245 b genome po
31	46	54.1	2258	2	O55459_9POTY	O55459 barley mild

RESULT 1

E3GL_ADE02

ID E3GL_ADE02 STANDARD; PRT; 159 AA.

AC P68978; P03251;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Early E3 18.5 kDa glycoprotein precursor (GP19K) (E3-19K) (E3gp 19-

DE kDa) (E19).

OS Human adenovirus 2 (HAdV-2).

OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

OX NCBI_TaxID=10515;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=81053687; PubMed=6253880;

RA Herise J., Courtois G., Galibert F.;

RT "Nucleotide sequence of the EcoRI D fragment of adenovirus 2 genome.;"

RL Nucleic Acids Res. 8:2173-2192(1980).

RN [2]

RP PROTEIN SEQUENCE OF N-TERMINUS, AND N-GLYCOSYLATION.

RX MEDLINE=85130985; PubMed=3882694;

RA Wold W.S.M., Cladaras C., Deutscher S.L., Kapoor Q.S.;

RT "The 19-kDa glycoprotein coded by region E3 of adenovirus.

RT Purification, characterization, and structural analysis.;"

RL J. Biol. Chem. 260:2424-2431(1985).

RN [3]

RP DISULFIDE BONDS, AND MUTAGENESIS OF CYS-28; CYS-39; CYS-45; CYS-100;

RP CYS-118; CYS-126 AND CYS-139.

RP PubMed=8057424;

RA Sester M., BURGERT H.-G.;

RT "Conserved cysteine residues within the E3/19K protein of adenovirus

RT type 2 are essential for binding to major histocompatibility complex

RT antigens.;"

RL J. Virol. 68:5423-5432(1994).

CC -I- FUNCTION: Binds and retains class I heavy chains in the

CC endoplasmic reticulum during the early period of virus infection,

CC thereby impairing their transport to the cell surface. Also delays

CC the expression of class I alleles that it cannot affect by direct

CC retention. Binds transporters associated with antigen processing

CC (TAP) and acts as a tapasin inhibitor, preventing class I/TAP

CC association. In consequence, infected cells are marked for immune

CC recognition by cytotoxic T lymphocytes (By similarity).

CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic

CC reticulum.

CC -I- DEVELOPMENTAL STAGE: Expressed at early period of virus infection.

CC -I- DOMAIN: The luminal domain binds directly to the peptide-binding

CC domain of class I molecules.

CC -I- PTM: Both disulfide bonds are absolutely critical for the

CC interaction with MHC antigens.

CC -I- PTM: N-glycosylated; high-mannose.

CC -I- SIMILARITY: Belongs to the adenoviruses E19 family.

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CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 CC EMBL; J01917; AAA92221.1; -; Genomic_DNA.
 CC PIR; A03821; Q6ADE.
 CC InterPro; IPR006965; Adeno_GPI9K.
 CC Pfam; PF04881; Adeno_GPI9K; 1.
 CC Direct protein sequencing; Early protein; Endoplasmic reticulum;
 KW Glycoprotein; Lectin; Mannose-binding; Membrane; Signal;
 KW Transmembrane; Viral immunoevasion.
 FT SIGNAL 1 17
 FT CHAIN 18 159 Early E3 18.5 kDa glycoprotein.
 FT TOPO DOM 18 123 Lumenal (Potential).
 FT TRANS MEM 124 144 Potential.
 FT TOPO DOM 145 159 Cytoplasmic (Potential).
 FT MOTIF 156 159 Mediates endoplasmic reticulum retention
 (By similarity).
 FT CARBOHYD 29 29 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 78 78 N-linked (GlcNAc. .) (Potential).
 FT DISULFID 28 45 Potential.
 FT DISULFID 39 100 Potential.
 FT MUTAGEN 28 28 C->S: Complete loss of binding to Tw1.3
 epitope.
 FT MUTAGEN 39 39 C->A,S: 60% loss of binding to Tw1.3
 epitope.
 FT MUTAGEN 45 45 C->S: Complete loss of binding to Tw1.3
 epitope.
 FT MUTAGEN 100 100 C->S: 60% loss of binding to Tw1.3
 epitope.
 FT MUTAGEN 118 118 C->S: No effect.
 FT MUTAGEN 126 126 C->S: No effect.
 FT MUTAGEN 139 139 C->S: No effect.
 SQ SEQUENCE 159 AA; 18438 MW; ED2519547E18AEB0 CRC64;

Query Match 100.0%; Score 85; DB 1; Length 159;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
 |||||
 Db 1 MRYMILGLLALAAVCSAA 18

RESULT 2
 E3GL_ADE06 STANDARD; PRT; 159 AA.
 AC P68979; P03251;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Early E3 18.5 kDa glycoprotein precursor (GPI9K) (E3-19K) (E3gp 19-
 kDa) (E19).
 OS Human adenovirus 6 (HAdV-6).
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 ON NCBI_TaxID=10534;
 RX [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Reichmann H., Schaarschmidt E., Geisler B., Hausmann J., Ortman D.,
 RA Bauer U., Flunker G., Seidel W.;
 RT "Sequence analysis of group C human adenoviruses type 1 and 6 for five
 genes of region E3.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Binds and retains class I heavy chains in the
 CC endoplasmic reticulum during the early period of virus infection,
 CC thereby impairing their transport to the cell surface. Also delays
 CC the expression of class I alleles that it cannot affect by direct
 CC retention. Binds transporters associated with antigen processing
 CC (TAP) and acts as a tapasin inhibitor, preventing class I/TAP
 CC association. In consequence, infected cells are masked for immune
 CC recognition by cytotoxic T lymphocytes (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic
 CC reticulum.

CC -!- DEVELOPMENTAL STAGE: Expressed at early period of virus infection.
 CC -!- DOMAIN: The lumenal domain binds directly to the peptide-binding
 CC domain of class I molecules.
 CC -!- PTM: Both disulfide bonds are absolutely critical for the
 CC interaction with MHC antigens (By similarity).
 CC -!- PTM: N-glycosylated; high-mannose (By similarity).
 CC -!- SIMILARITY: Belongs to the adenoviruses E3 family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; Y16037; CAA75990.1; -; Genomic_DNA.
 CC InterPro; IPR006965; Adeno_GPI9K.
 CC Pfam; PF04881; Adeno_GPI9K; 1.
 CC Early protein; Endoplasmic reticulum; Glycoprotein; Lectin;
 KW Mannose-binding; Membrane; Signal; Transmembrane; Viral immunoevasion.
 FT SIGNAL 1 17
 FT CHAIN 18 159 By similarity.
 FT TOPO DOM 18 123 Early E3 18.5 kDa glycoprotein.
 FT TRANS MEM 124 144 Lumenal (Potential).
 FT TOPO DOM 145 159 Potential.
 FT MOTIF 156 159 Cytoplasmic (Potential).
 (By similarity).
 FT CARBOHYD 29 29 Mediates endoplasmic reticulum retention
 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 78 78 N-linked (GlcNAc. .) (Potential).
 FT DISULFID 28 45 By similarity.
 FT DISULFID 39 100 By similarity.
 SQ SEQUENCE 159 AA; 18438 MW; ED2519547E18AEB0 CRC64;

Query Match 100.0%; Score 85; DB 1; Length 159;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
 |||||
 Db 1 MRYMILGLLALAAVCSAA 18

RESULT 3
 Q91024_ADE02 PRELIMINARY; PRT; 159 AA.
 AC Q91024;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE 19K glycoprotein.
 OS Human adenovirus 2 (HAdV-2).
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 ON NCBI_TaxID=10515;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liquor;
 RA Borchering F., Pring-Akerblom P.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ293915; CAC67720.1; -; Genomic DNA.
 DR GO; GO:0005537; F:mannose binding; IEA.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0005069; P:regulation of antiviral response by virus; IEA.
 DR InterPro; IPR006965; Adeno_GPI9K.
 DR Pfam; PF04881; Adeno_GPI9K; 1.
 SQ SEQUENCE 159 AA; 18411 MW; C2EDBA547E000DBA CRC64;

Query Match 100.0%; Score 85; DB 2; Length 159;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
 |||||
 Db 1 MRYMILGLLALAAVCSAA 18

```

DR GO; GO:0005537; F:mannose binding; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0005690; F:regulation of antiviral response by virus; IEA.
DR InterPro; IPR006965; AdenoGP19K.
DR Pfam; PF04881; AdenoGP19K_1.
SQ SEQUENCE 160 AA; 18518 MW; 09BFB37474631000 CRC64;

Query Match 75.3%; Score 64; DB 2; Length 160;
Best Local Similarity 72.2%; Pred. No. 0.19;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRYMILGLLAALAAVCSAA 18
   ::||| |||||
Db 2 IKYIILSLTLAAVCSAA 19

RESULT 6
Q75WH5_MACGS
ID Q75WH5_MACGS PRELIMINARY; PRT; 81 AA.
AC Q75WH5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Peptide toxin 2.
OS Macrochele gigas (Spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Araneae;
OC Mygalomorphae; Hexathelidae; Macrochele.
OX NCBI_TaxID=223896;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Venom gland;
RA Satake H., Villegas E., Corzo G.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB121196; BAD13403.1; -; mRNA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR011696; Toxin_12.
DR Pfam; PF07740; Toxin_12; 1.
DR SEQUENCE 81 AA; 9042 MW; 534E7162AC41ECFB CRC64;

Query Match 63.5%; Score 54; DB 2; Length 81;
Best Local Similarity 60.0%; Pred. No. 3.4;
Matches 12; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 1 MRY--MILGLLAALAAVCSAA 18
   |.:||| |||||
Db 1 MKYVMVILGLLVLAACCAS 20

RESULT 7
Q95P73_HABIR
ID Q95P73_HABIR PRELIMINARY; PRT; 179 AA.
AC Q95P73;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Thrombostasin (Fragment).
OS Haematobia irritans (Horn fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscoidea;
OC Muscidae; Haematobia.
OX NCBI_TaxID=7368;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Salivary gland;
RA MEDLINE=21663793; PubMed=11804804; DOI=10.1016/S0965-1748(01)00093-5;
RX Zhang D., Cupp M.S., Cupp E.W.;
RT "Thrombostasin: purification, molecular cloning and expression of a
RT novel anti-thrombin protein from horn fly saliva.";
RL Insect Biochem. Mol. Biol. 32:321-330 (2002).
DR EMBL; AF299078; AAK60013.1; -; mRNA.
FT NON TER
SQ SEQUENCE 179 AA; 19910 MW; 86710AE8A1ADC8FA CRC64;

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Query Match 60.0%; Score 51; DB 2; Length 179;
Best Local Similarity 53.3%; Pred. No. 17;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 YMIIGLLAALAVCSA 17
DB 8 FVIGILALSVCQA 22

RESULT 8
Q7QIDA ANOQA PRELIMINARY; PRT; 208 AA.
AC Q7QIDA;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ENSANGF0000013405 (Fragment).
GN ORFNames=ENSANGG0000010916;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008807; EAA04053.2; -; Genomic_DNA.
FT NON TER 208
SQ SEQUENCE 208 AA; 22236 MW; 0C842054742B1720 CRC64;

Query Match 60.0%; Score 51; DB 2; Length 208;
Best Local Similarity 44.4%; Pred. No. 19;
Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRYMILGLAALAVCSAA 18
DB 1 MKYSLVAVLIIAICSSA 18

RESULT 9
Q7U6K1 SYNXP PRELIMINARY; PRT; 294 AA.
AC Q7U6K1;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ABC transporter component, possibly Mn transport.
GN OrderedLocNames=SYN11337;
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J.,
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus."
RL Nature 424:1037-1042(2003).
DR EMBL; BX569692; CAF07852.1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001626; ABC_3.
DR Pfam; PF00950; ABC-3; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 294 AA; 31407 MW; BFE5B7C2598629D4 CRC64;

Query Match 60.0%; Score 51; DB 2; Length 294;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRYMILGLAALAAV 14
DB 187 LHYMLGLLSLAAY 200

RESULT 10
Q5FP07 GLUOX PRELIMINARY; PRT; 110 AA.
AC Q5FP07;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=GOX2153;
OS Gluconobacter oxydans (Gluconobacter suboxydans).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconobacter.
OX NCBI_TaxID=442;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=621H;
RX PubMed=15665824; DOI=10.1038/nbt1062;
RA Prust C., Hoffmeister M., Liesegang H., Wierzer A., Fricke W.F.,
RA Ehrenreich A., Gottschalk G., Deppenmeier U.;
RT "Complete genome sequence of the acetic acid bacterium Gluconobacter
RT oxydans."
RL Nat. Biotechnol. 23:195-200(2005).
DR EMBL; CP000009; AAW61889.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 110 AA; 11831 MW; 6366A71086B2E5A2 CRC64;

Query Match 57.6%; Score 49; DB 2; Length 110;
Best Local Similarity 61.1%; Pred. No. 23;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRYMILGLAALAVCSAA 18
DB 1 MRYVLLPSLLLSAASAA 18

RESULT 11
Q4USJ3 XANCP PRELIMINARY; PRT; 294 AA.
AC Q4USJ3;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Xc_2932;
OS Xanthomonas campestris pv. campestris str. 8004.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=314565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=8004;
RA Qian W., Jia Y.-T., Ren S.-X., He Y.-Q., Feng J.-X., Lu L.-F.,
RA Sun Q.-H., Ying G., Tang D.-J., Wu W., Wang L.-F., Jiang B.-L.,
RA Zeng S.-Y., Gu W.-Y., Lu G., Rong L., Tian Y.-C., Yao Z.-J., Fu G.,
RA Chen B.-S., Fang R.-X., Qiang B.-Q., Chen Z., Zhao G.-P., Tang J.-L.,
RA He C.-Z.;


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RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RA "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RN Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence";
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RN NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003826; AAF58647.3; -; Genomic_DNA.
DR EMBL; BT003225; AAO24980.1; -; mRNA.
DR HSP; P00441; 1P1V.
DR Ensembl; CG9027; Drosophila melanogaster.
DR FlyBase; FBgn0033631; CG9027.
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001424; SOD_CU_ZN.
DR Pfam; PF00080; SOD_Cu; 1.
DR PRINTS; PR00068; CUNDISMTASE.
DR PRODOM; PD000469; SOD_CU_ZN; 1.
DR PROSITE; PS00087; SOD_CU_ZN_1; 1.
DR PROSITE; PS00332; SOD_CU_ZN_2; 1.
KW Copper; Metal-binding; Oxidoreductase; Zinc.
SQ SEQUENCE 181 AA; 19221 MW; 68EACE43F8D05CA1 CRC64;

Query Match 56.5%; Score 48; DB 2; Length 181;
Best Local Similarity 44.4%; Pred. No. 47;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRYMILGGLAALAAVCSAA 18
Db |:::| |:::| |:::|
2 MQYLVVSLALCATICSAA 19

RESULT 14
Q95T42 DROME PRELIMINARY; PRT; 188 AA.
ID Q95T42;
AC Q95T42;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GH23708P.
DE ORFNames=CG9027;
GN Drosophila melanogaster (fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003826; AAF58647.3; -; Genomic_DNA.
DR EMBL; BT003225; AAO24980.1; -; mRNA.
DR HSP; P00441; 1P1V.
DR Ensembl; CG9027; Drosophila melanogaster.
DR FlyBase; FBgn0033631; CG9027.
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001424; SOD_CU_ZN.
DR Pfam; PF00080; SOD_Cu; 1.
DR PRINTS; PR00068; CUNDISMTASE.
DR PRODOM; PD000469; SOD_CU_ZN; 1.
DR PROSITE; PS00087; SOD_CU_ZN_1; 1.
DR PROSITE; PS00332; SOD_CU_ZN_2; 1.
KW Copper; Metal-binding; Oxidoreductase; Zinc.
SQ SEQUENCE 181 AA; 19221 MW; 68EACE43F8D05CA1 CRC64;

Query Match 56.5%; Score 48; DB 2; Length 181;
Best Local Similarity 44.4%; Pred. No. 47;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRYMILGGLAALAAVCSAA 18
Db |:::| |:::| |:::|
2 MQYLVVSLALCATICSAA 19

RESULT 14
Q95T42 DROME PRELIMINARY; PRT; 188 AA.
ID Q95T42;
AC Q95T42;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GH23708P.
DE ORFNames=CG9027;
GN Drosophila melanogaster (fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003826; AAF58647.3; -; Genomic_DNA.
DR EMBL; BT003225; AAO24980.1; -; mRNA.
DR HSP; P00441; 1P1V.
DR Ensembl; CG9027; Drosophila melanogaster.
DR FlyBase; FBgn0033631; CG9027.
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001424; SOD_CU_ZN.
DR Pfam; PF00080; SOD_Cu; 1.
DR PRINTS; PR00068; CUNDISMTASE.
DR PRODOM; PD000469; SOD_CU_ZN; 1.
DR PROSITE; PS00087; SOD_CU_ZN_1; 1.
DR PROSITE; PS00332; SOD_CU_ZN_2; 1.
KW Copper; Metal-binding; Oxidoreductase; Zinc.
SQ SEQUENCE 181 AA; 19221 MW; 68EACE43F8D05CA1 CRC64;
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RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY060339; AAL25378.1; -; mRNA.
DR HSP; P00441; 1P1V.
DR Ensembl; CG9027; Drosophila melanogaster.
DR FlyBase; FBgn0033631; CG9027.
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001424; SOD_CU_ZN.
DR Pfam; PF00080; SOD_Cu; 1.
DR PRINTS; PR00068; CUNDISMTASE.
DR PROSITE; PS00087; SOD_CU_ZN_1; 1.
DR PROSITE; PS00332; SOD_CU_ZN_2; 1.
KW Copper; Metal-binding; Oxidoreductase; Zinc.
SQ SEQUENCE 188 AA; 20069 MW; 94164B910821F909 CRC64;

Query Match 56.5%; Score 48; DB 2; Length 188;
Best Local Similarity 44.4%; Pred. No. 49;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRYMILGGLAALAAVCSAA 18
Db |:::| |:::| |:::|
9 MQYLVVSLALCATICSAA 26

RESULT 15
Q95U195 DROME PRELIMINARY; PRT; 250 AA.
ID Q95U195;
AC Q95U195;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE RE42883p (Fragment).
DE Name=CG9027;
GN Drosophila melanogaster (fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT015997; AAV36882.1; -; mRNA.
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001424; SOD_CU_ZN.
DR Pfam; PF00080; SOD_Cu; 1.
DR PRINTS; PR00068; CUNDISMTASE.
DR PRODOM; PD000469; SOD_CU_ZN; 1.
DR PROSITE; PS00087; SOD_CU_ZN_1; 1.
DR PROSITE; PS00332; SOD_CU_ZN_2; 1.
FT NON_TER 1
SQ SEQUENCE 250 AA; 26745 MW; 880274248DE41FCA CRC64;

Query Match 56.5%; Score 48; DB 2; Length 250;
Best Local Similarity 44.4%; Pred. No. 60;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRYMILGGLAALAAVCSAA 18
Db |:::| |:::| |:::|
35 MQYLVVSLALCATICSAA 52

Search completed: January 11, 2006, 00:09:39
Job time : 73 secs
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2006-01-11 12:26:42

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 11, 2006, 00:06:33 ; Search time 23 Seconds
(without alignments)
64.703 Million cell updates/sec

Title: US-10-031-008-7
Perfect score: 85
Sequence: 1 MRYWILGLLAALAAVCSSA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	27	1	US-08-464-318-7
2	85	100.0	27	1	US-08-471-341-7
3	85	100.0	27	1	US-08-461-566-7
4	85	100.0	27	2	US-09-070-629-2
5	85	100.0	90	2	US-09-124-671-25
6	85	100.0	109	2	US-09-124-671-23
7	85	100.0	109	2	US-09-124-671-27
8	85	100.0	109	2	US-09-124-671-29
9	81	95.3	17	1	US-08-464-318-1
10	81	95.3	17	1	US-08-471-341-1
11	81	95.3	17	1	US-08-461-566-1
12	80	94.1	31	2	US-09-653-182-74
13	51	60.0	175	2	US-09-376-113-7
14	51	60.0	175	2	US-10-200-659-7
15	48	56.5	128	2	US-09-270-767-41350
16	48	56.5	128	2	US-09-270-767-56566
17	47	55.3	305	2	US-09-902-540-13846
18	47	55.3	305	2	US-09-489-039A-7371
19	47	55.3	370	2	US-09-270-767-32759
20	47	55.3	370	2	US-09-270-767-47976
21	46	54.1	157	2	US-09-252-991A-22612
22	45	52.9	367	2	US-09-902-540-14540
23	44	51.8	485	2	US-09-328-352-8210
24	43.5	51.2	195	2	US-09-252-991A-22429
25	43	50.6	208	2	US-09-248-796A-14596
26	43	50.6	319	2	US-10-028-051A-8
27	42	49.4	168	2	US-09-376-113-5

28	42	49.4	168	2	US-10-200-659-5	Sequence 5, Appli
29	42	49.4	417	2	US-09-949-016-6482	Sequence 6482, Ap
30	42	49.4	471	2	US-09-893-737-186	Sequence 186, App
31	42	49.4	555	2	US-09-252-991A-31521	Sequence 31521, A
32	41	48.2	376	2	US-09-949-016-7545	Sequence 7545, Ap
33	41	48.2	482	2	US-09-489-039A-9528	Sequence 9528, Ap
34	40.5	47.6	254	2	US-09-270-767-44818	Sequence 44818, A
35	40.5	47.6	355	2	US-08-890-719-11	Sequence 11, Appl
36	40.5	47.6	355	2	US-08-890-719-13	Sequence 13, Appl
37	40	47.1	236	2	US-09-902-540-15029	Sequence 15029, A
38	40	47.1	274	2	US-09-540-236-2944	Sequence 2944, Ap
39	40	47.1	325	2	US-08-878-474-9	Sequence 9, Appli
40	40	47.1	325	2	US-09-576-594-479	Sequence 479, App
41	40	47.1	325	2	US-10-014-055-2	Sequence 2, Appli
42	40	47.1	325	2	US-10-014-055-4	Sequence 4, Appli
43	40	47.1	325	2	US-10-028-051A-2	Sequence 2, Appli
44	40	47.1	325	2	US-10-028-051A-4	Sequence 4, Appli
45	40	47.1	371	2	US-09-949-016-7544	Sequence 7544, Ap

ALIGNMENTS

RESULT 1
US-08-464-318-7
; Sequence 7, Application US/08464318
; Patent No. 5733548
; GENERAL INFORMATION:
; APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,
; APPLICANT: STEVEN A., BENNINK, JACK R., BACIK, IGOR,
; APPLICANT: YEWDELL, JONATHAN W
; TITLE OF INVENTION: IMMUNOGENIC CHIMERAS
; TITLE OF INVENTION: COMPRISING NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: ENDOPLASMIC RETICULUM SIGNAL SEQUENCE
; TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND
; TITLE OF INVENTION: THEIR USES IN VACCINES AND DISEASE TREATMENTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,318
; FILING DATE: 5-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/032,902
; FILING DATE: 17-MAR-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4069US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-08-464-318-7
Query Match 100.0%; Score 85; DB 1; Length 27;

Best Local Similarity 100.0%; Pred. No. 1.7e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 1 MRYMILGLLALAAVCSAA 18
| | | | | | | | | | | | | | | | | |
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 2

US-08-471-341-7
; Sequence 7, Application US/08471341
; Patent No. 5846540
; GENERAL INFORMATION:
; APPLICANT: RESTIPO, NICHOLAS P., ROSENBERG,
; APPLICANT: STEVEN A., BENNINK, JACK R., BACIK, IGOR,
; APPLICANT: YEWDELL, JONATHAN W.
; TITLE OF INVENTION: IMMUNOGENIC CHIMERAS
; TITLE OF INVENTION: COMPRISING NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: ENDOPLASMIC RETICULUM SIGNAL SEQUENCE
; TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND
; TITLE OF INVENTION: THEIR USES IN VACCINES AND DISEASE TREATMENTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,341
; FILING DATE:
; CLASSIFICATION: 514

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/032,902
; FILING DATE: 17-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4069
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; TELEX: 421792

INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-08-471-341-7

Query Match 100.0%; Score 85; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
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Db 1 MRYMILGLLALAAVCSAA 18

RESULT 3

US-08-461-566-7
; Sequence 7, Application US/08461566
; Patent No. 5856187
; GENERAL INFORMATION:
; APPLICANT: RESTIPO, NICHOLAS P., ROSENBERG,
; APPLICANT: STEVEN A., BENNINK, JACK R., BACIK, IGOR,
; APPLICANT: YEWDELL, JONATHAN W.

; TITLE OF INVENTION: IMMUNOGENIC CHIMERAS
; TITLE OF INVENTION: COMPRISING NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: ENDOPLASMIC RETICULUM SIGNAL SEQUENCE
; TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND
; TITLE OF INVENTION: THEIR USES IN VACCINES AND DISEASE TREATMENTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,566
; FILING DATE: 05-JUNE-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/032,902
; FILING DATE: 17-MAR-1993
; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4069US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; TELEX: 421792

INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-08-461-566-7

Query Match 100.0%; Score 85; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
| | | | | | | | | | | | | | | | | |
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 4

US-09-070-629-2
; Sequence 2, Application US/09070629
; Patent No. 6984414
; GENERAL INFORMATION:
; APPLICANT: Palese, P.
; APPLICANT: Garcia-Sastre, A.
; APPLICANT: Restifo, N.
; TITLE OF INVENTION: RECOMBINANT INFLUENZA VIRUSES EXPRESSING
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGENS AS ANTITUMOR AGENTS
; FILE REFERENCE: 6923-071
; CURRENT APPLICATION NUMBER: US/09/070,629
; CURRENT FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: 60/045,176
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Leader peptide

; OTHER INFORMATION: and beta-gal epitope

US-09-070-629-2

Query Match 100.0%; Score 85; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMIGLLAALAAVCSAA 18
Db 1 MRYMIGLLAALAAVCSAA 18

RESULT 5

US-09-124-671-25
; Sequence 25, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human PLB-KDEL
US-09-124-671-25

Query Match 100.0%; Score 85; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMIGLLAALAAVCSAA 18
Db 1 MRYMIGLLAALAAVCSAA 18

RESULT 6

US-09-124-671-23
; Sequence 23, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human COMP-KDEL
US-09-124-671-23

Query Match 100.0%; Score 85; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMIGLLAALAAVCSAA 18
Db 1 MRYMIGLLAALAAVCSAA 18

RESULT 7

US-09-124-671-27
; Sequence 27, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human TSP3-KDEL
US-09-124-671-27

Query Match 100.0%; Score 85; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMIGLLAALAAVCSAA 18
Db 1 MRYMIGLLAALAAVCSAA 18

RESULT 8

US-09-124-671-29
; Sequence 29, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human TSP4-KDEL
US-09-124-671-29

Query Match 100.0%; Score 85; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMIGLLAALAAVCSAA 18
Db 1 MRYMIGLLAALAAVCSAA 18

RESULT 9

US-08-464-318-1
; Sequence 1, Application US/08464318
; Patent No. 5733548
; GENERAL INFORMATION:
; APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,
; APPLICANT: STEVEN A., BENNING, JACK R., BACIK, IGOR,
; APPLICANT: YEWDELL, JONATHAN W
; TITLE OF INVENTION: IMMUNOGENIC CHIMERAS
; TITLE OF INVENTION: COMPRISING NUCLEIC ACID SEQUENCES ENCODING

;/ TITLE OF INVENTION: ENDOPLASMIC RETICULUM SIGNAL SEQUENCE
;/ TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND
;/ NUMBER OF SEQUENCES: 14
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: MORGAN & FINNEGAN
;/ STREET: 345 PARK AVENUE
;/ CITY: NEW YORK
;/ COUNTRY: U.S.A.
;/ ZIP: 10154
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette
;/ COMPUTER: IBM PC COMPATIBLE
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: WORD PERFECT 5.1
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/464,318
;/ FILING DATE: 5-JUNE-1995
;/ CLASSIFICATION: 514
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/032,902
;/ FILING DATE: 17-MAR-1993
;/ CLASSIFICATION: 514
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: RICHARD W. BORK
;/ REGISTRATION NUMBER: 36,459
;/ REFERENCE/DOCKET NUMBER: 2026-4069US2
;/ TELEPHONE: 212-758-4800
;/ TELEFAX: 212-751-6849
;/ TELEX: 421792
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 17 amino acid residues
;/ TYPE: amino acid
;/ STRANDEDNESS: unknown
;/ TOPOLOGY: unknown
;/ US-08-464-318-1
;/
;/ Query Match 95.3%; Score 81; DB 1; Length 17;
;/ Best Local Similarity 100.0%; Pred. No. 4.6e-07;
;/ Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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;/ QY 1 MRYMILGLLALAAVCSA 17
;/ Db 1 MRYMILGLLALAAVCSA 17
;/
;/ RESULT 10
;/ US-08-471-341-1
;/ Sequence 1, Application US/08471341
;/ Patent No. 5846540
;/ GENERAL INFORMATION:
;/ APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,
;/ APPLICANT: STEVEN A., BENNINK, JACK R., BACIK, IGOR,
;/ APPLICANT: YEWDELL, JONATHAN W.
;/ TITLE OF INVENTION: IMMUNOGENIC CHIMERAS
;/ TITLE OF INVENTION: COMPRISING NUCLEIC ACID SEQUENCES ENCODING
;/ TITLE OF INVENTION: ENDOPLASMIC RETICULUM SIGNAL SEQUENCE
;/ TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND
;/ TITLE OF INVENTION: THEIR USES IN VACCINES AND DISEASE TREATMENTS
;/ NUMBER OF SEQUENCES: 14
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: MORGAN & FINNEGAN
;/ STREET: 345 PARK AVENUE
;/ CITY: NEW YORK
;/ COUNTRY: U.S.A.
;/ ZIP: 10154
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette
;/ COMPUTER: IBM PC COMPATIBLE
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: WORD PERFECT 5.1
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/461,566
;/ FILING DATE: 05-JUNE-1995
;/ CLASSIFICATION: 424
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/032,902
;/ FILING DATE: 17-MAR-1993
;/ CLASSIFICATION: 424
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: RICHARD W. BORK
;/ REGISTRATION NUMBER: 36,459
;/ REFERENCE/DOCKET NUMBER: 2026-4069US3
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 212-758-4800
;/ TELEFAX: 212-751-6849
;/ TELEX: 421792
;/

;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/471,341
;/ FILING DATE:
;/ CLASSIFICATION: 514
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/032,902
;/ FILING DATE: 17-MAR-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: RICHARD W. BORK
;/ REGISTRATION NUMBER: 36,459
;/ REFERENCE/DOCKET NUMBER: 2026-4069
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 212-758-4800
;/ TELEFAX: 212-751-6849
;/ TELEX: 421792
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 17 amino acid residues
;/ TYPE: amino acid
;/ STRANDEDNESS: unknown
;/ TOPOLOGY: unknown
;/ US-08-471-341-1
;/
;/ Query Match 95.3%; Score 81; DB 1; Length 17;
;/ Best Local Similarity 100.0%; Pred. No. 4.6e-07;
;/ Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;/
;/ QY 1 MRYMILGLLALAAVCSA 17
;/ Db 1 MRYMILGLLALAAVCSA 17
;/
;/ RESULT 11
;/ US-08-461-566-1
;/ Sequence 1, Application US/08461566
;/ Patent No. 5856187
;/ GENERAL INFORMATION:
;/ APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,
;/ APPLICANT: STEVEN A., BENNINK, JACK R., BACIK, IGOR,
;/ APPLICANT: YEWDELL, JONATHAN W.
;/ TITLE OF INVENTION: IMMUNOGENIC CHIMERAS
;/ TITLE OF INVENTION: COMPRISING NUCLEIC ACID SEQUENCES ENCODING
;/ TITLE OF INVENTION: ENDOPLASMIC RETICULUM SIGNAL SEQUENCE
;/ TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND
;/ TITLE OF INVENTION: THEIR USES IN VACCINES AND DISEASE TREATMENTS
;/ NUMBER OF SEQUENCES: 14
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: MORGAN & FINNEGAN
;/ STREET: 345 PARK AVENUE
;/ CITY: NEW YORK
;/ COUNTRY: U.S.A.
;/ ZIP: 10154
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette
;/ COMPUTER: IBM PC COMPATIBLE
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: WORD PERFECT 5.1
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/461,566
;/ FILING DATE: 05-JUNE-1995
;/ CLASSIFICATION: 424
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/032,902
;/ FILING DATE: 17-MAR-1993
;/ CLASSIFICATION: 424
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: RICHARD W. BORK
;/ REGISTRATION NUMBER: 36,459
;/ REFERENCE/DOCKET NUMBER: 2026-4069US3
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 212-758-4800
;/ TELEFAX: 212-751-6849
;/ TELEX: 421792
;/

```
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 17 amino acid residues
;   TYPE: amino acid
;   STRANDEDNESS: unknown
;   TOPOLOGY: unknown
US-08-461-566-1

Query Match          95.3%; Score 81; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAACVCSA 17
   |||||
Db 1 MRYMILGLLALAACVCSA 17

RESULT 12
US-09-653-182-74
; Sequence 74, Application US/09653182
; Patent No. 6881825
; GENERAL INFORMATION:
; APPLICANT: Paul D. Robbins
; APPLICANT: Zhibao Mi
; APPLICANT: Raymond Frizzell
; APPLICANT: Joseph C. Gloriosio
; APPLICANT: Andrea Gambotto
; TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT FACILITATE
; TITLE OF INVENTION: UPTAKE AND CYTOPLASMIC AND/OR NUCLEAR TRANSPORT
; TITLE OF INVENTION: OF PROTEINS, DNA AND VIRUSES
; FILE REFERENCE: AP32573-A-A
; CURRENT APPLICATION NUMBER: US/09/653,182
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,980
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/188,944
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: random peptide library
US-09-653-182-74

Query Match          94.1%; Score 80; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYMILGLLALAACVCSA 18
   |||||
Db 15 RYMILGLLALAACVCSA 31

RESULT 13
US-09-376-113-7
; Sequence 7, Application US/09376113
; Patent No. 6451992
; GENERAL INFORMATION:
; APPLICANT: Cupp, Eddie Wayne
; APPLICANT: Cupp, Mary Smith
; TITLE OF INVENTION: Antithrombin Nucleotides and Proteins
; TITLE OF INVENTION: from Horn Fly
; FILE REFERENCE: 5721-10
; CURRENT APPLICATION NUMBER: US/09/376,113
; CURRENT FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Haematobia Irritans
US-09-376-113-7

Query Match          60.0%; Score 51; DB 2; Length 175;
Best Local Similarity 53.3%; Pred. No. 0.67;
Matches 8; Conservative 6; Mismatches 0; Indels 1; Gaps 0;

QY 3 YMILGLLALAACVCSA 17
   :::::
Db 4 FVVIGILALSVCQA 18

RESULT 14
US-10-200-659-7
; Sequence 7, Application US/10200659
; Patent No. 6927279
; GENERAL INFORMATION:
; APPLICANT: Cupp, Eddie Wayne
; APPLICANT: Cupp, Mary Smith
; TITLE OF INVENTION: Antithrombin Nucleotides and Proteins
; TITLE OF INVENTION: from Horn Fly
; FILE REFERENCE: 5721-10
; CURRENT APPLICATION NUMBER: US/10/200,659
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/376,113
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Haematobia Irritans
US-10-200-659-7

Query Match          60.0%; Score 51; DB 2; Length 175;
Best Local Similarity 53.3%; Pred. No. 0.67;
Matches 8; Conservative 6; Mismatches 0; Indels 1; Gaps 0;

QY 3 YMILGLLALAACVCSA 17
   :::::
Db 4 FVVIGILALSVCQA 18

RESULT 15
US-09-270-767-41350
; Sequence 41350, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41350
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-41350

Query Match          56.5%; Score 48; DB 2; Length 128;
Best Local Similarity 53.3%; Pred. No. 1.5;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAACV 15
   :::::
Db 72 IRYWVIGTVALLLVC 86

Search completed: January 11, 2006, 00:10:38
Job time : 23 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 11, 2006, 00:09:44 ; Search time 61 Seconds
(without alignments)
123.294 Million cell updates/sec

Title: US-10-031-008-7
Perfect score: 85
Sequence: 1 MRYMILGLLALAAVCSAA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	18	3	US-09-894-594-65
2	85	100.0	18	3	US-09-894-594-70
3	85	100.0	18	4	US-10-080-797-13
4	85	100.0	27	5	US-10-848-620-2
5	85	100.0	90	4	US-10-815-514-25
6	85	100.0	90	5	US-10-877-930-25
7	85	100.0	90	5	US-10-873-594-25
8	85	100.0	109	4	US-10-815-514-23
9	85	100.0	109	4	US-10-815-514-27
10	85	100.0	109	4	US-10-815-514-29
11	85	100.0	109	5	US-10-877-930-23
12	85	100.0	109	5	US-10-877-930-27
13	85	100.0	109	5	US-10-877-930-29
14	85	100.0	109	5	US-10-873-594-23
15	85	100.0	109	5	US-10-873-594-27
16	85	100.0	109	5	US-10-873-594-29
17	82	96.5	26	4	US-10-331-163-2
18	80	94.1	31	4	US-10-075-869-74
19	80	94.1	31	4	US-10-366-493-74
20	80	94.1	31	5	US-10-926-893-74
21	51	60.0	175	4	US-10-200-659-7
22	48	56.5	179	6	US-11-097-143-19317
23	48	56.5	181	6	US-11-097-143-28680
24	46	54.1	140	4	US-10-156-761-8319
25	46	54.1	148	4	US-10-424-599-216653
26	46	54.1	5175	4	US-10-120-801-74
27	46	54.1	5175	4	US-10-369-493-6859

Sequence 6861, Ap
Sequence 75, Appl
Sequence 6858, Ap
Sequence 6860, Ap
Sequence 34, Appl
Sequence 253783,
Sequence 22, Appl
Sequence 33, Appl
Sequence 240570,
Sequence 78114, A
Sequence 69847, A
Sequence 43294, A
Sequence 213064,
Sequence 149240,
Sequence 42052, A
Sequence 32480, A
Sequence 1, Appli
Sequence 2692, Ap

46 54.1 5175 4 US-10-369-493-6861
46 54.1 5198 4 US-10-120-801-75
46 54.1 5198 4 US-10-369-493-6858
46 54.1 5198 4 US-10-369-493-6860
46 54.1 5198 4 US-10-346-863-34
45 52.9 84 4 US-10-425-115-253783
34 45 52.9 3390 5 US-10-719-547-22
35 45 52.9 3390 5 US-10-871-775-33
36 44 51.8 154 4 US-10-425-115-240570
37 44 51.8 372 4 US-10-282-122A-78114
38 44 51.8 406 4 US-10-425-114-69847
39 44 51.8 485 4 US-10-425-114-43294
40 44 51.8 525 4 US-10-425-115-213064
41 43 50.6 108 4 US-10-424-599-149240
42 42 49.4 62 4 US-10-767-701-42052
43 42 49.4 72 4 US-10-767-701-32480
44 42 49.4 100 4 US-10-283-656-1
45 42 49.4 100 5 US-10-723-860-2692

ALIGNMENTS

RESULT 1

US-09-894-594-65
; Sequence 65, Application US/09894594
; Publication No. US20030017497A1
; GENERAL INFORMATION:
; APPLICANT: Kleber-Emmons, Thomas
; APPLICANT: Weiner, David B.
; APPLICANT: Monzavi-Karbassi, Behjatolah
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Enc.
; TITLE OF INVENTION: Same
; FILE REFERENCE: UPN-3984
; CURRENT APPLICATION NUMBER: US/09/894,594
; PRIOR FILING DATE: 2001-06-28
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: PCT/US99/02405
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/073,690
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/214,517
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Novel Sequence
US-09-894-594-65

Query Match 100.0%; Score 85; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e+06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
| | | | | | | | | | | | | | | | | |
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 2

US-09-894-594-70
; Sequence 70, Application US/09894594
; Publication No. US20030017497A1
; GENERAL INFORMATION:
; APPLICANT: Kleber-Emmons, Thomas
; APPLICANT: Weiner, David B.
; APPLICANT: Monzavi-Karbassi, Behjatolah
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Enc

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; TITLE OF INVENTION: Same
; FILE REFERENCE: UPN-3984
; CURRENT APPLICATION NUMBER: US/09/894,594
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/601,558
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: PCT/US99/02405
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/073,690
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/214,517
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Novel Sequence
US-09-894-594-70

Query Match          100.0%; Score 85; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 3
US-10-080-797-13
; Sequence 13, Application US/10080797
; Publication No. US20020183253A1
; GENERAL INFORMATION:
; APPLICANT: Campochiaro, Peter A.
; APPLICANT: Dixon, Katharine H.
; APPLICANT: Brazzell, Romulus K.
; TITLE OF INVENTION: METHOD FOR TREATING OCULAR
; TITLE OF INVENTION: NEOVASCULARIZATION
; FILE REFERENCE: 4-31881A
; CURRENT APPLICATION NUMBER: US/10/080,797
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Adenovirus
US-10-080-797-13

Query Match          100.0%; Score 85; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 4
US-10-848-620-2
; Sequence 2, Application US/10848620
; Publication No. US20040253273A1
; GENERAL INFORMATION:
; APPLICANT: Palese, P.
; APPLICANT: Garcia-Sastre, A.
; APPLICANT: Restifo, N.
; TITLE OF INVENTION: RECOMBINANT INFLUENZA VIRUSES EXPRESSING
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGENS AS ANTITUMOR AGENTS
; FILE REFERENCE: 6923-071

; CURRENT APPLICATION NUMBER: US/10/848,620
; CURRENT FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: US/09/070,629
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/045,176
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Leader peptide
; OTHER INFORMATION: and beta-gal epitope
US-10-848-620-2

Query Match          100.0%; Score 85; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 5
US-10-815-514-25
; Sequence 25, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/815,514
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human PLB-KDEL
US-10-815-514-25

Query Match          100.0%; Score 85; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 6
US-10-877-930-25
; Sequence 25, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
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; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human PLB-KDEL
US-10-877-930-25

Query Match      100.0%; Score 85; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRYMILGLLALAAVCSAA 18
      |||||
Db      1 MRYMILGLLALAAVCSAA 18

RESULT 7
US-10-873-594-25
; Sequence 25, Application US/10873594
; Publication No. US20050095667A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: A31488-I-1 065360.0152
; CURRENT APPLICATION NUMBER: US/10/873,594
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/09/800,358
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/696,070
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: 09/124,671
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric KDEL receptor inhibitor

; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: Cleavable leader/signal peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(3)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (6)...(9)
; OTHER INFORMATION: The sub-sequence GDCC
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (10)...(36)
; OTHER INFORMATION: human PLB pentamerization domain
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (13)...(13)
; OTHER INFORMATION: Critical for pentamer formation
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (18)...(18)
; OTHER INFORMATION: Critical for pentamer formation
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (21)...(21)
; OTHER INFORMATION: Critical for pentamer formation

; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (24)...(24)
; OTHER INFORMATION: Critical for pentamer formation
; FEATURE:
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; LOCATION: (28)...(28)
; OTHER INFORMATION: Critical for pentamer formation
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (31)...(31)
; OTHER INFORMATION: Critical for pentamer formation
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (37)...(60)
; OTHER INFORMATION: Camel IgG linker domain
US-10-873-594-25

Query Match      100.0%; Score 85; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRYMILGLLALAAVCSAA 18
      |||||
Db      1 MRYMILGLLALAAVCSAA 18

RESULT 8
US-10-815-514-23
; Sequence 23, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/815,514
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human COMP-KDEL
US-10-815-514-23

Query Match      100.0%; Score 85; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRYMILGLLALAAVCSAA 18
      |||||
Db      1 MRYMILGLLALAAVCSAA 18

RESULT 9
US-10-815-514-27
; Sequence 27, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/815,514
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
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; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human TSP3-KDEL
US-10-815-514-27

Query Match      100.0%; Score 85; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 10
US-10-815-514-29
; Sequence 29, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/815,514
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human TSP4-KDEL
US-10-815-514-29

Query Match      100.0%; Score 85; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 11
US-10-877-930-23
; Sequence 23, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human TSP3-KDEL
US-10-877-930-23

Query Match      100.0%; Score 85; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 12
US-10-877-930-27
; Sequence 27, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human TSP3-KDEL
US-10-877-930-27

Query Match      100.0%; Score 85; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 13
US-10-877-930-29
; Sequence 29, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human TSP4-KDEL
US-10-877-930-29

Query Match      100.0%; Score 85; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 MRYMILGLLALAAVCSAA 18
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 14
US-10-873-594-23
; Sequence 23, Application US/10873594
; Publication No. US20050095667A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: A31488-I-I 065360.0152
; CURRENT APPLICATION NUMBER: US/10/873,594
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/09/800,358
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/696,070
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: 09/124,671
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric KDEL receptor inhibitor
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: Cleavable leader/signal peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(3)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (6)...(9)
; OTHER INFORMATION: The sub-sequence GDCC
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (10)...(55)
; OTHER INFORMATION: human COMP pentamerization domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (56)...(79)
; OTHER INFORMATION: Camel IgG linker domain
US-10-873-594-23

Query Match 100.0%; Score 85; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
Db 1 MRYMILGLLALAAVCSAA 18

RESULT 15
US-10-873-594-27
; Sequence 27, Application US/10873594
; Publication No. US20050095667A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: A31488-I-I 065360.0152

; CURRENT APPLICATION NUMBER: US/10/873,594
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/09/800,358
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/696,070
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: 09/124,671
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric KDEL receptor inhibitor
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: Cleavable leader/signal peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(3)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (6)...(9)
; OTHER INFORMATION: The sub-sequence GDCC
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (10)...(55)
; OTHER INFORMATION: human TSP3 trimerization domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (56)...(79)
; OTHER INFORMATION: Camel IgG linker domain
US-10-873-594-27

Query Match 100.0%; Score 85; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAAVCSAA 18
Db 1 MRYMILGLLALAAVCSAA 18

Search completed: January 11, 2006, 00:19:38
Job time : 62 secs

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OM protein - protein search, using sw model

Run on: January 11, 2006, 00:10:09 ; Search time 8 seconds
(without alignments)
19.111 Million cell updates/sec

Title: US-10-031-008-7
Perfect score: 85
Sequence: 1 MRYMILGLLALAAVCSSA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 61141 seqs, 8493638 residues

Total number of hits satisfying chosen parameters: 61141

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap:
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap:
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap:
4: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pap:
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap:
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap:
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap:
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	50.6	319	7 US-11-184-005-8	Sequence 8, Appli
2	41	48.2	152	7 US/11/020	Sequence 31, Appl
3	40	47.1	325	7 US-11-184-005-2	Sequence 2, Appli
4	40	47.1	325	7 US-11-184-005-4	Sequence 4, Appli
5	40	47.1	824	6 US-10-821-234-1008	Sequence 1008, Ap
6	39	45.9	74	7 US-11-000-463-819	Sequence 819, App
7	39	45.9	74	7 US-11-000-463-820	Sequence 820, App
8	39	45.9	331	7 US-11-143-980-57	Sequence 57, Appl
9	39	45.9	502	7 US-11-102-240-158	Sequence 158, App
10	39	45.9	1061	7 US-11-000-463-347	Sequence 347, App
11	39	45.9	1091	7 US-11-000-463-348	Sequence 348, App
12	38	44.7	163	7 US-11-102-240-160	Sequence 160, App
13	37.5	44.1	618	7 US-11-078-735-18	Sequence 18, Appl
14	37	43.5	243	6 US-10-821-234-1661	Sequence 1661, Ap
15	37	43.5	243	6 US-10-878-556A-118	Sequence 118, App
16	37	43.5	861	6 US-10-467-657-1286	Sequence 1286, Ap
17	36	42.4	143	7 US-11-186-284-117	Sequence 117, App
18	36	42.4	350	6 US-10-873-528-132	Sequence 132, App
19	36	42.4	390	6 US-10-131-826A-338	Sequence 338, App
20	36	42.4	548	6 US-10-055-877-320	Sequence 320, App
21	36	42.4	675	6 US-10-055-877-117	Sequence 117, App
22	36	42.4	146	7 US-11-000-463-881	Sequence 881, App
23	35	41.2	146	7 US-11-000-463-881	Sequence 881, App
24	35	41.2	158	7 US-11-097-622-10	Sequence 10, Appl
25	35	41.2	181	7 US-11-000-463-409	Sequence 409, App

Sequence 157, App
Sequence 159, App
Sequence 174, App
Sequence 88, Appl
Sequence 87, Appl
Sequence 1436, Ap
Sequence 2644, Ap
Sequence 4376, Ap
Sequence 239, App
Sequence 28, Appl
Sequence 67, Appl
Sequence 44, Appl
Sequence 321, App
Sequence 240, App
Sequence 241, App
Sequence 90, Appl
Sequence 225, App
Sequence 1694, Ap
Sequence 105, App

26 35 41.2 193 7 US-11-186-284-157
27 35 41.2 193 7 US-11-186-284-159
28 35 41.2 238 6 US-10-623-155-174
29 35 41.2 325 7 US-11-129-143-88
30 35 41.2 331 7 US-11-129-143-87
31 35 41.2 377 6 US-10-821-234-1436
32 35 41.2 445 6 US-10-793-626-2644
33 35 41.2 494 6 US-10-467-657-4376
34 35 41.2 619 7 US-11-205-109-30
35 35 41.2 622 6 US-10-055-877-239
36 35 41.2 628 7 US-11-094-519A-28
37 35 41.2 635 6 US-10-055-877-67
38 35 41.2 640 7 US-11-094-519A-44
39 35 41.2 673 6 US-10-055-877-321
40 35 41.2 885 6 US-10-055-877-240
41 35 41.2 885 6 US-10-055-877-241
42 35 41.2 1005 7 US-11-080-991-90
43 34.5 40.6 271 7 US-11-052-554A-225
44 34 40.0 82 6 US-10-821-234-1694
45 34 40.0 186 6 US-10-873-528-105

ALIGNMENTS

RESULT 1
US-11-184-005-8
; Sequence 8, Application US/11184005
; Publication No. US20050256052A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; APPLICANT: Moos, Malcolm JR.
; APPLICANT: Hoang, Bang
; APPLICANT: Wang, Shouwen
; TITLE OF INVENTION: METHOD OF MODULATING TISSUE
; FILE REFERENCE: NIH133.1CPC3
; CURRENT APPLICATION NUMBER: US/11/184,005
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 10/028051
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 08/822333
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: US 08/729,452
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-11-184-005-8
Query Match 50.6%; Score 43; DB 7; Length 319;
Best Local Similarity 66.7%; Pred. No. 3.6;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 4 MILGLLAAVC 15
:: |||||:
Db 10 LLAGLLAALC 21
RESULT 2
US/11/020
; Sequence 31, Application US/11020772
; Publication No. US20050256043A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig, Linda B.
; TITLE OF INVENTION: HIV Antisense Proteins
; FILE REFERENCE: 25125.0001
; CURRENT APPLICATION NUMBER: US/11/020,772


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; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 09/249,542
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,640
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 08/853,703
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 31
; LENGTH: 152
; TYPE: PRT
; ORGANISM: human immunodeficiency virus of Clade A
; FEATURE:
; OTHER INFORMATION: HIV antisense HAP protein translated from AUG start; requires -1
US/11/020,772-31

Query Match      48.2%; Score 41; DB 7; Length 152;
Best Local Similarity 46.7%; Pred. No. 3.5;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY      4 MILGLLALAAVCSAA 18
Db      102 MLVGWISLALVCNSA 116
      |:::|::|::|::|::|

RESULT 3
US-11-184-005-2
; Sequence 2, Application US/11184005
; Publication No. US20050256052A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; APPLICANT: Moos, Malcolm JR.
; APPLICANT: Hoang, Bang
; APPLICANT: Wang, Shouwen
; TITLE OF INVENTION: METHOD OF MODULATING TISSUE
; FILE REFERENCE: NIH133-1CPC3
; CURRENT APPLICATION NUMBER: US/11/184,005
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 10/028051
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 08/822333
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: US 08/729,452
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Bos taurus
US-11-184-005-2

Query Match      47.1%; Score 40; DB 7; Length 325;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      7 GLLALAAVC 15
Db      15 GLLALAAVC 23
      |||||::|

RESULT 4
US-11-184-005-4
; Sequence 4, Application US/11184005
; Publication No. US20050256052A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; APPLICANT: Moos, Malcolm JR.
; APPLICANT: Hoang, Bang
; APPLICANT: Wang, Shouwen
; TITLE OF INVENTION: METHOD OF MODULATING TISSUE
; FILE REFERENCE: NIH133-1CPC3
; CURRENT APPLICATION NUMBER: US/11/184,005
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 10/028051
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 08/822333
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: US 08/729,452
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Bos taurus
US-11-184-005-4

Query Match      47.1%; Score 40; DB 7; Length 325;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      7 GLLALAAVC 15
Db      15 GLLALAAVC 23
      |||||::|

RESULT 5
US-10-821-234-1008
; Sequence 1008, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1008
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1008

Query Match      47.1%; Score 40; DB 6; Length 824;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY      6 LGLLALAAVCSA 17
Db      55 LGLLALAAVAAA 66
      |||||::|

RESULT 6
US-11-000-463-819
; Sequence 819, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong B.
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
```

```
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 819
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-11-000-463-819

Query Match 45.9%; Score 39; DB 7; Length 74;
Best Local Similarity 50.0%; Pred. No. 3.4;
Matches 6; Conservative 5; Mismatches 1; Indels 1; Gaps 0;

QY 4 MTLGLLAAVVC 15
|::|||::|
DB 1 MVLGIVAAALC 12

RESULT 7
US-11-000-463-820
; Sequence 820, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chonghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 820
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; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-11-000-463-820

Query Match 45.9%; Score 39; DB 7; Length 74;
Best Local Similarity 50.0%; Pred. No. 3.4;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 MTLGLLAAVVC 15
|::|||::|
DB 1 MVLGIVAAALC 12

RESULT 8
US-11-143-980-57
; Sequence 57, Application US/11143980
; Publication No. US20050272133A1
; GENERAL INFORMATION:
; APPLICANT: He, Min
; APPLICANT: Hucul, John
; APPLICANT: Haltli, Bradley A.
; APPLICANT: Wagenaar, Melissa M.
; APPLICANT: Graziani, Edmund
; APPLICANT: Summers, Mia
; APPLICANT: Kulowski, Kerry
; APPLICANT: Pong, Kevin
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
; TITLE OF INVENTION: Polyketide
; FILE REFERENCE: AM-101426US
; CURRENT APPLICATION NUMBER: US/11/143,980
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/664,483
; PRIOR FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US 60/576,895
; PRIOR FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Streptomyces sp.
;
US-11-143-980-57

Query Match 45.9%; Score 39; DB 7; Length 331;
Best Local Similarity 56.2%; Pred. No. 16;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 YMTLGLLAAVCSAA 18
|::|||::|
DB 192 YLGNGLLAAVCSAA 207

RESULT 9
US-11-102-240-158
; Sequence 158, Application US/11102240
; Publication No. US20050260647A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRES
; TITLE OF INVENTION: ESOPHAGEAL TUMOR
; FILE REFERENCE: P3230R1C106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 10/063662
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
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; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 158
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-102-240-158
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Query Match 45.9%; Score 39; DB 7; Length 502;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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QY 4 MTLGLLAAVCSAA 18
| | | | | | | | | | | | | | | | | |
Db 1 MSLVLLSLAALCRSA 15
```

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RESULT 10
US-11-000-463-347
; Sequence 347, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
```

```
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
```

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; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
```

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; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1061
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-347
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Query Match 45.9%; Score 39; DB 7; Length 1061;
Best Local Similarity 50.0%; Pred. No. 56;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
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QY 4 MTLGLLAAVCSAA 15
| | | | | | | | | | | | | | | | | |
Db 988 MVGVIVAAAALC 999
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RESULT 11
US-11-000-463-348
; Sequence 348, Application US/11000463
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; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
```

```
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
```

```
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-348
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Query Match 45.9%; Score 39; DB 7; Length 1091;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
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QY 4 MTLGLLAAVCSAA 15
| | | | | | | | | | | | | | | | | |
Db 1018 MVGVIVAAAALC 1029
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```
RESULT 12
US-11-102-240-160
; Sequence 160, Application US/11102240
; Publication No. US20050260647A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRES-
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; FILE REFERENCE: P3230RIC106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 10/063662
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 160
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; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-102-240-160

Query Match      44.7%; Score 38; DB 7; Length 163;
Best Local Similarity 38.9%; Pred. No. 11;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAACSAA 18
Db 12 VKYLLLSILGLAFLESA 29

RESULT 13
US-11-078-735-18
; Sequence 18, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn ver. 3.3
; SEQ ID NO 18
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-18

Query Match      44.1%; Score 37.5; DB 7; Length 618;
Best Local Similarity 50.0%; Pred. No. 56;
Matches 10; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 2 RYMI---LGLLALAACSAA 18
Db 490 RYLLPPALGLLVAGVAGAA 509

RESULT 14
US-10-821-234-1661
; Sequence 1661, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1661
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1661

Query Match      43.5%; Score 37; DB 6; Length 243;
Best Local Similarity 46.7%; Pred. No. 25;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAACVC 15
Db 105 LRYKLGLGLAVRRAC 119

RESULT 15
US-10-878-556A-118
; Sequence 118, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/rs3_human
; DATABASE ENTRY DATE: 1991-11-01
US-10-878-556A-118

Query Match      43.5%; Score 37; DB 6; Length 243;
Best Local Similarity 46.7%; Pred. No. 25;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRYMILGLLALAACVC 15
Db 105 LRYKLGLGLAVRRAC 119

Search completed: January 11, 2006, 00:19:57
Job time : 9 secs
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